```
=> d his nofile
```

```
(FILE 'HOME' ENTERED AT 09:54:26 ON 05 SEP 2006)
    FILE 'CAPLUS' ENTERED AT 09:54:40 ON 05 SEP 2006
               SET LINE 250
               SET DETAIL OFF
               E US1999-235416/AP, PRN 25
               SET LINE LOGIN
               SET DETAIL LOGIN
L1
             1 SEA ABB=ON US99-235416/PRN
               D SCAN
L2
            45 SEA ABB=ON SAKOWICZ R?/AU
          1091 SEA ABB=ON GOLDSTEIN L?/AU
L3
            61 SEA ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR TL/OBI) (W) GAMMA/OBI
T.4
               E TEST KITS+ALL/CT
L5
        17063 SEA ABB=ON TEST KITS/CT
             9 SEA ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)
L6
          1841 SEA ABB=ON KINESINS/CT
L7
             2 SEA ABB=ON THERMOMYCES LANUGINOSUS/CT(L)GAMMA/OBI
L8
         20619 SEA ABB=ON MICROTUBULE#/OBI
L9
          3352 SEA ABB=ON MOTOR/OBI(L)PROTEIN#/OBI
L10
     FILE 'REGISTRY' ENTERED AT 09:59:03 ON 05 SEP 2006
               E PROTEIN KINASE/CN
L11
             1 SEA ABB=ON "PROTEIN KINASE"/CN
    FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006
               D IDE
    FILE 'CAPLUS' ENTERED AT 09:59:35 ON 05 SEP 2006
          97768 SEA ABB=ON L11 OR PROTEIN KINASE#/OBI
L12
             O SEA ABB=ON L8 NOT L4
L13
             1 SEA ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)
L14
           220 SEA ABB=ON L7 AND L9 AND L10
L15
           161 SEA ABB=ON L9(L)L10 AND L7
L16
            48 SEA ABB=ON END DIRECT?/OBI
L17
             3 SEA ABB=ON L15 AND L17
L18
               E SCREENING/CT
         42502 SEA ABB=ON L12(L) (MODULAT?/OBI OR INHIBIT?/OBI OR ACTIVAT?/OBI
L19
               )
L20
            11 SEA ABB=ON L15 AND L19
             0 SEA ABB=ON L16 AND L19
L21
               D QUE L20
               D SCAN TI L20
             1 SEA ABB=ON MAP/TI AND L20
L22
               D SCAN
           477 SEA ABB=ON L19(L)ANST/RL
L23
            3 SEA ABB=ON L15 AND L23
L24
           233 SEA ABB=ON L19 AND L5
L25
               D SCA L1
L26
            20 SEA ABB=ON L7 AND L25
               D QUE
L27
             8 SEA ABB=ON L7 AND L25 AND L23
               D SCAN TI
    FILE 'WPIX' ENTERED AT 10:38:16 ON 05 SEP 2006
           36 SEA ABB=ON SAKOWICZ R?/AU
L28
           64 SEA ABB=ON GOLDSTEIN L?/AU
L29
```

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- - -
                     1 SEA ABB=ON (THERMOMYCES LANUGINOSUS/BI, ABEX OR TL/BI, ABEX) (A) G
L30
                        AMMA/BI, ABEX
                        D TRIAL
                     3 SEA ABB=ON L28 AND L29
L31
                        D TRIAL 1-3
                D TRIAL 1-3

252 SEA ABB=ON KINESIN#/BI,ABEX

811 SEA ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,ABEX

120 SEA ABB=ON MOTOR PROTEIN#/BI,ABEX

1863 SEA ABB=ON END DIRECT?/BI,ABEX

4006 SEA ABB=ON PROTEIN KINASE#/BI,ABEX

105 SEA ABB=ON L32 AND L33 OR L34 OR L35)

54 SEA ABB=ON L32 AND L33 AND L34

3 SEA ABB=ON L32 AND L33 AND L34

3 SEA ABB=ON L32 AND L36

2492 SEA ABB=ON L36 (3A) (MODULAT?/BI,ABEX OR INHIBIT?/BI,ABEX OR ACTIVAT?/BI,ABEX)
L32
L33
L34
L35
L36
L37
L38
L39
L40
L41
                        ACTIVAT?/BI,ABEX)
L42
                      3 SEA ABB=ON L32 AND L41
                        D TRIAL 1-3
              302435 SEA ABB=ON SCREEN?/BI,ABEX
L43
                 1372 SEA ABB=ON DRUG#/BI, ABEX (2A) CANDIDATE#/BI, ABEX
L44
                  484 SEA ABB=ON L41 AND (L43 OR L44)
15 SEA ABB=ON L41 AND L43 AND L44
L45
L46
                        D TRIAL 1-5
                        D OUE
                    45 SEA ABB=ON L41 AND (L33 OR L34 OR L35)
L47
                      9 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L43 OR L44)
L48
                         D TRIAL 1-3
                         D TRIAL L31 1-3
        FILE 'STNGUIDE' ENTERED AT 10:52:47 ON 05 SEP 2006
        FILE 'WPIX' ENTERED AT 10:58:19 ON 05 SEP 2006
                11026 SEA ABB=ON L43(2A)(DRUG#/BI,ABEX OR COMPOUND#/BI,ABEX)
L49
                      2 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L44 OR L49)
L50
                         D TRIAL 1-2
                         D KWIC 1-2
                    38 SEA ABB=ON L41(S)((L44 OR L49))
L51
                    19 SEA ABB=ON L41(10A)((L44 OR L49))
15 SEA ABB=ON L41(5A)((L44 OR L49))
0 SEA ABB=ON L51 AND (L33 OR L34 OR L35)
L52
L53
L54
        FILE 'STNGUIDE' ENTERED AT 11:01:44 ON 05 SEP 2006
        FILE 'WPIX' ENTERED AT 11:02:37 ON 05 SEP 2006
               50839 SEA ABB=ON ASSAY#/BI,ABEX
3543 SEA ABB=ON L43(3A)L55
26 SEA ABB=ON L56 AND (L49 OR L44) AND L41
1 SEA ABB=ON L57 AND (L33 OR L34 OR L35)
2 SEA ABB=ON L56 (S) (L49 OR L44) (S) L41
L55
L56
L57
L58
L59
        INDEX '1MOBILITY, 2MOBILITY, ABI-INFORM, ADISCTI, AEROSPACE, AGRICOLA,
```

ALUMINIUM, ANABSTR, ANTE, APOLLIT, AQUALINE, AQUASCI, AQUIRE, BABS, BIBLIODATA, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAOLD, CAPLUS, CASREACT, CBNB, CEABA-VTB, CERAB, ... 'ENTERED AT 11:05:41 ON 05 SEP 2006

SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

- 8 FILE AEROSPACE
- 1 FILE AGRICOLA
- 11 FILE ANABSTR

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Hines 09/235416 search history
     FILE AQUASCI
 1
     FILE BIOENG
 3
     FILE BIOSIS
14
     FILE BIOTECHNO
 2
     FILE CABA
 1
     FILE CAOLD
     FILE CAPLUS
63
     FILE CIVILENG
 1
     FILE COMPENDEX
46
     FILE COMPUSCIENCE
 2
     FILE CONFSCI
 1
     FILE DDFU
 1
     FILE DGENE
     FILE DISSABS
 5
     FILE DRUGU
 1
     FILE EMBAL
 2
     FILE EMBASE
16
     FILE ENERGY
150
     FILE ENVIROENG
 1
     FILE EPFULL
 9
     FILE ESBIOBASE
 9
     FILE GBFULL
 2
     FILE GENBANK
 2
     FILE GEOREF
 1
     FILE HEALSAFE
 3
     FILE IFIPAT
 6
     FILE INIS
152
     FILE INPADOC
     FILE INSPEC
176
     FILE INSPHYS
10
     FILE JAPIO
 1
16
     FILE JICST-EPLUS
     FILE LIFESCI
 3
 3
     FILE MECHENG
11
      FILE MEDLINE
     FILE METADEX
 6
      FILE NTIS
33
21
      FILE PASCAL
      FILE PATDPAFULL
 9
      FILE PCTFULL
12
      FILE POLLUAB
 5
      FILE SCISEARCH
58
     FILE SOLIDSTATE
 1
     FILE TEMA
 6
     FILE TOXCENTER
21
     FILE TULSA
 1
     FILE ULIDAT
 1
     FILE USPATFULL
19
```

FILE 'STNGUIDE' ENTERED AT 11:10:58 ON 05 SEP 2006

FILE USPAT2 FILE WPIDS FILE WPINDEX

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 11:15:21 ON 05 SEP 2006

QUE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

L61 138 SEA ABB=ON SAKOWICZ R?/AU

```
4782 SEA ABB=ON GOLDSTEIN L?/AU
147 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL)(A) GAMMA
L62
L63
               147 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMI
13861 SEA ABB=ON KINESIN#
132140 SEA ABB=ON MICROTUBULE# OR MICRO TUBULE#
7756 SEA ABB=ON MOTOR PROTEIN#
2654 SEA ABB=ON END DIRECT?
40 SEA ABB=ON (L61 AND L62) OR ((L61 OR L62) AND L63)
L64
L65
L66
L67
L68
                      22 DUP REM L68 (18 DUPLICATES REMOVED)
L69
                                    ANSWERS '1-2' FROM FILE DRUGU
                                    ANSWER '3' FROM FILE PASCAL
                                    ANSWERS '4-5' FROM FILE BIOTECHNO
                                    ANSWERS '6-17' FROM FILE BIOSIS
                                    ANSWER '18' FROM FILE LIFESCI
                                    ANSWERS '19-20' FROM FILE CONFSCI
                                    ANSWERS '21-22' FROM FILE SCISEARCH
           ANSWERS '21-22' FROM FILE SCISEARCH

567385 SEA ABB=ON PROTEIN KINASE#

3 SEA ABB=ON L63 AND (L64 OR L65 OR L66 OR L67 OR L70)

377 SEA ABB=ON L64 AND L65 AND L66 AND L67

83 SEA ABB=ON L64 AND L65 (5A) L66 (5A) L67

12 SEA ABB=ON L64 (3A) L65 (3A) L66 (3A) L67

20 SEA ABB=ON L64 (5A) L65 (5A) L66 (5A) L67

262577 SEA ABB=ON L70 (3A) ((MODULAT? OR INHIBIT? OR ACTIVAT?))

2376 SEA ABB=ON (SCREEN? OR CANDIDATE#) (3A) (DRUG# OR COMPOUND#) (5A)
L70
L71
L72
L73
L74
L75
L76
L77
                             ASSAY?
                      0 SEA ABB=ON L76 (S) L77 AND (L64 OR L65 OR L66 OR L67)
12 SEA ABB=ON L76 (S) L77
L78
L79
        FILE 'MEDLINE' ENTERED AT 11:23:32 ON 05 SEP 2006
                     13 SEA ABB=ON SAKOWICZ R?/AU
L80
                   1168 SEA ABB=ON GOLDSTEIN L?/AU
11 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
4 SEA ABB=ON (L80 AND L81) OR ((L80 OR L81) AND L82)
L81
L82
L83
                           D TRIAL 1-4
                            E KINESIN+ALL/CT
                   2094 SEA ABB=ON KINESIN/CT
L84
                            E MICROTUBULES+ALL/CT
                 17967 SEA ABB=ON MICROTUBULES/CT
76212 SEA ABB=ON ENZYME INHIBITORS/CT
L85
L86
                            E MOTOR PROTEIN/CT
                   1529 SEA ABB=ON MOTOR PROTEIN#
359 SEA ABB=ON END DIRECT?
0 SEA ABB=ON L82 AND (L84 OR L85 OR L86 OR L87 OR L88)
L87
L88
L89
                            D TRIAL L82 1-3
                            D TRIAL L82 4-11
                    325 SEA ABB=ON L84 AND L85 AND (L87 OR L88)
34 SEA ABB=ON L84 AND L85 AND L87 AND L88
9 SEA ABB=ON L87(8A)L88 AND L84 AND L85
L90
L91
T.92
                            E PROTEIN KINASE/CT
                            E E3+ALL
               184405 SEA ABB=ON PROTEIN KINASES+NT/CT
L93
                            E SCREENING/CT
                            E E4+ALL
                 22924 SEA ABB=ON DRUG EVALUATION, PRECLINICAL/CT
102 SEA ABB=ON L93 AND L94 AND L86
64 SEA ABB=ON L93/MAJ AND L94 AND L86/MAJ
13 SEA ABB=ON L93/MAJ AND L94(L)MT/CT AND L86/MAJ
L94
L95
L96
1.97
                            D TRIAL 1-4
L98
                 28397 SEA ABB=ON L93(L)AI/CT
                  8557 SEA ABB=ON L98/MAJ
L99
                 21967 SEA ABB=ON ENZYME ACTIVATION/CT(L)DE/CT
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189 SEA ABB=ON L100/MAJ
L101
              19 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L94(L)MT/CT
L102
             4668 SEA ABB=ON L94(L)MT/CT
L103
         1977 SEA ABB=ON L103/MAJ
L104
               10 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L104
L105
                  D TRIAL 1-3
                0 SEA ABB=ON L95 AND L84
L106
     FILE 'EMBASE' ENTERED AT 11:33:37 ON 05 SEP 2006
             13 SEA ABB=ON SAKOWICZ R?/AU
L107
              922 SEA ABB=ON GOLDSTEIN L?/AU
L108
              16 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
5 SEA ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)
L109
L110
                  D TRIAL 1-5
      FILE 'STNGUIDE' ENTERED AT 11:34:20 ON 05 SEP 2006
     FILE 'EMBASE' ENTERED AT 12:01:08 ON 05 SEP 2006
                5 SEA.ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)
L111
                  D TRIAL 1-5
            2142 SEA ABB=ON KINESIN/CT
3476 SEA ABB=ON MICROTUBULE ASSEMBLY/CT
754 SEA ABB=ON MICROTUBULE PROTEIN/CT
L112
L113
L114
           13611 SEA ABB=ON MICROTUBULE/CT
316 SEA ABB=ON END DIRECT?
L115
L116
                  E MOTOR PROTEIN/CT
                  E E3+ALL
              569 SEA ABB=ON MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L117
                0 SEA ABB=ON L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
L118
                  L117)
                7 SEA ABB=ON L112 AND (L113 OR L114 OR L115) AND L116 AND L117
L119
                  E ENZYME ACTIVAT/CT
           68045 SEA ABB=ON ENZYME ACTIVATION/CT 1083 SEA ABB=ON ENZYME ACTIVATOR/CT
L120
L121
                  E ENZYME MODULAT/CT
           39 SEA ABB=ON ENZYME MODULATION/CT
16880 SEA ABB=ON ENZYME INHIBITOR/CT
89209 SEA ABB=ON ENZYME INHIBITION/CT
L122
L123
L124
                  E PROTEIN KINASE/CT
           20757 SEA ABB=ON PROTEIN KINASE+NT/CT
2690 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR
L125
L126
                  L124)
               31 SEA ABB=ON L126 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
L127
                  L117 OR L109)
L128
                4 SEA ABB=ON GENERAL REVIEW/DT AND L127
                  D TRIAL 1-4
                  E ENZYME ACTIVITY/CT
L129
          221084 SEA ABB=ON ENZYME ACTIVITY/CT
                  E DRUG SCREENING/CT
                  E E3+ALL
L130
           74504 SEA ABB=ON 'DRUG SCREENING/CT
                  E E19+ALL
L131
           22260 SEA ABB=ON SCREENING TEST/CT
L132
            4100 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR L124
                  OR L129)
L133
               24 SEA ABB=ON L132 AND (L130 OR L131)
                  D TRIAL 1-4
            4072 SEA ABB=ON PROTEIN KINASE INHIBITOR/CT
1431 SEA ABB=ON L134/MAJ
L134 '
L135
```

53 SEA ABB=ON L135 AND (L130 OR L131)

```
71 SEA ABB=ON L133 OR L136
L137
                E ANALYTIC METHOD+ALL/CT
                D QUE L137
L138
              1 SEA ABB=ON L137 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
                L117 OR L109)
     FILE 'STNGUIDE' ENTERED AT 12:12:41 ON 05 SEP 2006
                D OUE L105
                D OUE L92
                D OUE L79
                D OUE L75
                D OUE L58
                D OUE L59
                D OUE L40
                D QUE L24
                D QUE L27
                D QUE L18
     FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006
                D QUE L1
                D OUE L6
L139
              9 SEA ABB=ON L1 OR L6
     FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006
                D QUE L31
     FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
     ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
     AT 12:14:50 ON 05 SEP 2006
                D QUE L68
     FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006
                D QUE L83
     FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006
                D QUE L110
     FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, BIOSIS,
     ESBIOBASE, LIFESCI, CONFSCI, SCISEARCH' ENTERED AT 12:15:12 ON 05 SEP 2006
L140
             26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)
                     ANSWERS '1-4' FROM FILE MEDLINE
                     ANSWERS '5-10' FROM FILE CAPLUS
                     ANSWERS '11-21' FROM FILE BIOSIS
                     ANSWER '22' FROM FILE LIFESCI
                     ANSWERS '23-24' FROM FILE CONFSCI
                     ANSWERS '25-26' FROM FILE SCISEARCH
                D IBIB ED ABS 1-26
     FILE 'STNGUIDE' ENTERED AT 12:15:40 ON 05 SEP 2006
                D OUE L14
                D OUE L18
                D QUE L30
                D QUE L39
                D QUE L40
                D OUE L71
                D QUE L75
     FILE 'CAPLUS' ENTERED AT 12:17:36 ON 05 SEP 2006
```

D OUE L14

O SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:17:38 ON 05 SEP 2006 D OUE L30

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:17:40 ON 05 SEP 2006

D OUE L71

L142 0 SEA ABB=ON L71 NOT L68 '

FILE 'MEDLINE' ENTERED AT 12:17:48 ON 05 SEP 2006 D QUE L89

FILE 'EMBASE' ENTERED AT 12:17:50 ON 05 SEP 2006 D QUE L118

FILE 'CAPLUS' ENTERED AT 12:19:00 ON 05 SEP 2006 D QUE L14

L143 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:19:01 ON 05 SEP 2006 D QUE L30

L144 0 SEA ABB=ON L30 NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:19:04 ON 05 SEP 2006

D QUE L71

L145 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006 D QUE L89

FILE 'EMBASE' ENTERED AT 12:19:14 ON 05 SEP 2006 D QUE L118

FILE 'STNGUIDE' ENTERED AT 12:19:27 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006 D QUE L18

L146 3 SEA ABB=ON L18 NOT L139

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006

D QUE L39

D QUE L40

L147 3 SEA ABB=ON (L39 OR L40) NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:21:01 ON 05 SEP 2006

D QUE L75

L148 20 SEA ABB=ON L75 NOT L68

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006 D QUE L92

L149 9 SEA ABB=ON L92 NOT L83

FILE 'EMBASE' ENTERED AT 12:21:12 ON 05 SEP 2006 D QUE L119

L150 7 SEA ABB=ON L119 NOT L110

FILE 'STNGUIDE' ENTERED AT 12:21:21 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, BIOTECHNO, BIOSIS, ESBIOBASE,

LIFESCI, SCISEARCH' ENTERED AT 12:21:44 ON 05 SEP 2006 L151

28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)

ANSWERS '1-9' FROM FILE MEDLINE

ANSWERS '10-12' FROM FILE CAPLUS

ANSWERS '13-15' FROM FILE WPIX

ANSWERS '16-21' FROM FILE EMBASE

ANSWERS '22-23' FROM FILE BIOTECHNO

ANSWERS '24-27' FROM FILE BIOSIS

ANSWER '28' FROM FILE LIFESCI

D IALL 1-9

D IBIB ED ABS HITIND 10-12

D IALL ABEQ TECH 13-15

D IALL 16-28

FILE 'STNGUIDE' ENTERED AT 12:22:44 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:24:49 ON 05 SEP 2006

D OUE L24

D OUE L27

L152 11 SEA ABB=ON (L24 OR L27) NOT (L18 OR L139)

FILE 'WPIX' ENTERED AT 12:24:50 ON 05 SEP 2006

D QUE L58

D QUE L59

3 SEA ABB=ON (L58 OR L59) NOT (L39 OR L40 OR L31) L153

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:24:53 ON 05 SEP 2006

D OUE L79

L154 12 SEA ABB=ON L79 NOT (L75 OR L68)

FILE 'MEDLINE' ENTERED AT 12:25:02 ON 05 SEP 2006

D OUE L105

10 SEA ABB=ON L105 NOT (L92 OR L83) L155

FILE 'EMBASE' ENTERED AT 12:25:03 ON 05 SEP 2006

D QUE L138

L156 1 SEA ABB=ON L138 NOT (L119 OR L110)

FILE 'STNGUIDE' ENTERED AT 12:25:10 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, ESBIOBASE' ENTERED AT 12:25:33 ON 05 SEP 2006

L157 34 DUP REM L155 L152 L153 L156 L154 (3 DUPLICATES REMOVED)

> ANSWERS '1-10' FROM FILE MEDLINE ANSWERS '11-21' FROM FILE CAPLUS

ANSWERS '22-24' FROM FILE WPIX

ANSWER '25' FROM FILE EMBASE

ANSWERS '26-27' FROM FILE DRUGU

ANSWERS '28-29' FROM FILE BIOTECHNO

ANSWERS '30-34' FROM FILE ESBIOBASE

D IALL 1-10

D IBIB ED ABS HITIND 11-21

D IALL ABEQ TECH 22-24

D IALL 25-34

=> fil reg; d ide FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2006 American Chemical Society (ACS)

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STRUCTURE FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4 DICTIONARY FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH June 30, 2006

Please note that search-term pricing does apply when conducting SmartSELECT searches.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

- L11 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2006 ACS on STN
- RN 372092-80-3 REGISTRY
- ED Entered STN: 28 Nov 2001
- CN Kinase (phosphorylating), protein (9CI) (CA INDEX NAME)

OTHER NAMES:

- CN Neurokinase
- CN Protein kinase
- MF Unspecified
- CI MAN
- SR CA
- LC STN Files: BIOSIS, CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
- *** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
 - 1917 REFERENCES IN FILE CA (1907 TO DATE)
 - 17 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 - 1930 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> =>

Page 2

=> fil capl; d que l1; d que l6
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FILE COVERS 1907 - 5 Sep 2006 VOL 145 ISS 11 FILE LAST UPDATED: 4 Sep 2006 (20060904/ED)

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'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

Inventor search

1 SEA FILE=CAPLUS ABB=ON US99-235416/PRN

L2 45 SEA FILE=CAPLUS ABB=ON SAKOWICZ R?/AU
L3 1091 SEA FILE=CAPLUS ABB=ON GOLDSTEIN L?/AU
L4 61 SEA FILE=CAPLUS ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR
TL/OBI) (W) GAMMA/OBI
L6 9 SEA FILE=CAPLUS ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)

=> s 11 or 16

L139 9 L1 OR L6

=> fil wpix; d que 131

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FILE LAST UPDATED: 1 SEP 2006 <20060901/UP>
MOST RECENT DERWENT UPDATE: 200656 <200656/DW>
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L28 36 SEA FILE=WPIX ABB=ON SAKOWICZ R?/AU
L29 64 SEA FILE=WPIX ABB=ON GOLDSTEIN L?/AU
L31 3 SEA FILE=WPIX ABB=ON L28 AND L29

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 168

138 SEA SAKOWICZ R?/AU L61 4782 SEA GOLDSTEIN L?/AU L62

147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA L63 40 SEA (L61 AND L62) OR ((L61 OR L62) AND L63) 1.68

=> fil medl; d que 183

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>). See also:

http://www.nlm.nih.gov/mesh/

http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L80	13 SEA FILE=MEDLINE ABB=ON	SAKOWICZ R?/AU
L81	1168 SEA FILE=MEDLINE ABB=ON	GOLDSTEIN L?/AU
L82	11 SEA FILE=MEDLINE ABB=ON	(THERMOMYCES LANUGINOSUS OR TL) (A) GAMM
	A	
L83	4 SEA FILE=MEDLINE ABB=ON	(L80 AND L81) OR ((L80 OR L81) AND
	L82)	

=> fil embase; d que 1110

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FILE COVERS 1974 TO 5 Sep 2006 (20060905/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

EMBASE is now updated daily. SDI frequency remains weekly (default) and biweekly.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L107 13 SEA FILE=EMBASE ABB=ON SAKOWICZ R?/AU
L108 922 SEA FILE=EMBASE ABB=ON GOLDSTEIN L?/AU
L109 16 SEA FILE=EMBASE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L110 5 SEA FILE=EMBASE ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)

=> dup rem 183,1139,131,1110,168
FILE 'MEDLINE' ENTERED AT 12:15:12 ON 05 SEP 2006

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PROCESSING COMPLETED FOR L83
PROCESSING COMPLETED FOR L139
PROCESSING COMPLETED FOR L31
PROCESSING COMPLETED FOR L110
PROCESSING COMPLETED FOR L68
L140

26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)
ANSWERS '1-4' FROM FILE MEDLINE

ANSWERS '1-4' FROM FILE MEDLINE
ANSWERS '5-10' FROM FILE CAPLUS
ANSWERS '11-21' FROM FILE BIOSIS
ANSWER '22' FROM FILE LIFESCI

ANSWERS '23-24' FROM FILE CONFSCI ANSWERS '25-26' FROM FILE SCISEARCH

=> d ibib ed abs 1-26

L140 ANSWER 1 OF 26 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 2000095847 MEDLINE DOCUMENT NUMBER: PubMed ID: 10631986

TITLE: Cloning and expression of kinesins from the thermophilic

fungus Thermomyces lanuginosus.

AUTHOR: Sakowicz R; Farlow S; Goldstein L S

CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Cellular and

Molecular Medicine, School of Medicine, University of

California, San Diego, La Jolla 92093-0683, USA.

CONTRACT NUMBER: GM35252 (NIGMS)

SOURCE: Protein science : a publication of the Protein Society,

(1999 Dec) Vol. 8, No. 12, pp. 2705-10. Journal code: 9211750. ISSN: 0961-8368.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200002

ENTRY DATE: Entered STN: 29 Feb 2000

Last Updated on STN: 29 Feb 2000 Entered Medline: 14 Feb 2000

ED Entered STN: 29 Feb 2000

Last Updated on STN: 29 Feb 2000 Entered Medline: 14 Feb 2000

The motor domain regions of three novel members of the kinesin superfamily TLKIF1, TLKIFC, and TLBIMC were identified in a thermophilic fungus Thermomyces lanuginosus. Based on sequence similarity, they were classified as members of the known kinesin families Unc104/KIF1, KAR3, and BIMC. TLKIF1 was subsequently expressed in Escherichia coli. The expression level was high, and the protein was mostly soluble, easy to purify, and enzymatically active. TLKIF1 is a monomeric kinesin motor, which in a gliding motility assay displays a robust plus-directed microtubule movement up to 2 microm/s. The discovery of TLKIF1 also demonstrates that a family of kinesin motors not previously found in fungi may in fact be used in this group of organisms.

L140 ANSWER 2 OF 26 MEDLINE on STN DUPLICATE 7

ACCESSION NUMBER: 1998202613 MEDLINE DOCUMENT NUMBER: PubMed ID: 9535660

TITLE: A marine natural product inhibitor of kinesin motors.

AUTHOR: Sakowicz R; Berdelis M S; Ray K; Blackburn C L;

CORPORATE SOURCE: Department of Pharmacology, Division of Cellular and

Molecular Medicine, Howard Hughes Medical Institute,

University of California, San Diego, 9500 Gilman Drive, La

Jolla, CA 92093-0683, USA.

SOURCE: Science, (1998 Apr 10) Vol. 280, No. 5361, pp. 292-5.

Journal code: 0404511. ISSN: 0036-8075.

Hopmann C; Faulkner D J; Goldstein L S

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199804

ENTRY DATE: Entered STN: 7 May 1998

Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998

ED Entered STN: 7 May 1998

Last Updated on STN: 7 May 1998 Entered Medline: 28 Apr 1998

AB Members of the kinesin superfamily of motor proteins are essential for mitotic and meiotic spindle organization, chromosome segregation, organelle and vesicle transport, and many other processes that require microtubule-based transport. A compound, adociasulfate-2, was isolated from a marine sponge, Haliclona (also known as Adocia) species, that inhibited kinesin activity by targeting its motor domain and mimicking the activity of the microtubule. Thus, the kinesin-microtubule interaction site could be a useful target for small molecule modulators, and adociasulfate-2 should serve as an archetype for specific inhibitors of kinesin functions.

L140 ANSWER 3 OF 26 MEDLINE on STN DUPLICATE 9

ACCESSION NUMBER: 1998028574 MEDLINE

DOCUMENT NUMBER: PubMed ID: 9363944

TITLE: CENP-E is a plus end-directed kinetochore motor required

for metaphase chromosome alignment.

AUTHOR: Wood K W; Sakowicz R; Goldstein L S;

Cleveland D W

CORPORATE SOURCE: Laboratory of Cell Biology, Ludwig Institute for Cancer

Research, University of California at San Diego, La Jolla

92093-0660, USA.

SOURCE: Cell, (1997 Oct 31) Vol. 91, No. 3, pp. 357-66.

Journal code: 0413066. ISSN: 0092-8674.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF027728

ENTRY MONTH: 199712

ENTRY DATE: Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998 Entered Medline: 10 Dec 1997

ED Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998 Entered Medline: 10 Dec 1997

AB Mitosis requires dynamic attachment of chromosomes to spindle microtubules. This interaction is mediated largely by kinetochores. During prometaphase, forces exerted at kinetochores, in combination with polar ejection forces, drive congression of chromosomes to the metaphase plate. A major question has been whether kinetochore-associated microtubule motors play an important role in congression. Using immunodepletion from and antibody addition to Xenopus egg extracts, we show that the kinetochore-associated kinesin-like motor protein CENP-E is essential for positioning chromosomes at the metaphase plate. We further demonstrate that CENP-E powers movement toward microtubule plus ends in vitro. These findings support a model in which CENP-E functions in congression to tether kinetochores to dynamic microtubule plus ends.

L140 ANSWER 4 OF 26 MEDLINE on STN

ACCESSION NUMBER: 96196874 MEDLINE

DOCUMENT NUMBER: PubMed ID: 8612068

TITLE: The muscle in kinesin.

AUTHOR: Sakowicz R; Goldstein L S

SOURCE: Nature structural biology, (1996 May) Vol. 3, No. 5, pp.

404-7.

Journal code: 9421566. ISSN: 1072-8368.

PUB. COUNTRY: United States
DOCUMENT TYPE: News Announcement

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199606

ENTRY DATE: Entered STN: 13 Jun 1996

Last Updated on STN: 13 Jun 1996

Entered Medline: 3 Jun 1996

ED Entered STN: 13 Jun 1996

Last Updated on STN: 13 Jun 1996

Entered Medline: 3 Jun 1996

L140 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 1999:487304 CAPLUS

DOCUMENT NUMBER: 131:112405

TITLE: Identification and expression of the microtubule motor

protein kinesin TL-γ

INVENTOR(S): Sakowicz, Roman; Goldstein, Lawrence S.

в.

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 75 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PAT	CENT I	NO.			KIN)	DATE		1	APPL:	ICAT:	ION 1	NO.		D	ATE	
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WO	9937	659			A1		1999	0729	Ţ	NO 1	999-1	US13!	55		1:	9990:	122
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		ĐK,	EE,	ES,	FI,	GB,	GD,	GE,	GH,	GM,	HR,	ΗU,	ID,	IL,	IN,	IS,	JP,
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		MW,	MX,	NO,	NZ,	PL,	PT,	RO,	ŔŪ,	SD,	SE,	SG,	SI,	SK,	SL,	ТJ,	TM,
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US	6815	169			B1		2004	1109	1	JS 2	000-	7246	66		2	0001	128 <
US	6764	830			В1		2004	0720	1	JS 2	000-	6008	23		2	0001	221 <
PRIORITY	Y APP	LN.	INFO	. :					1	US 1:	998-	7236	1P	1	A2 1	9980	123
									1	JS 1	999-	2354	16	1	A3 1	9990	122 <
									1	WO 1	999-1	US13	55	1	W 1	9990	122

ED Entered STN: 06 Aug 1999

The invention concerns the isolation of a nucleic acid sequence from Thermomyces lanuginosus that encodes the microtubule motor protein kinesin TL- γ with the following properties: the protein's activity includes plus end-directed microtubule motor activity; the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL- γ tail domain as measured using a sequence comparison algorithm; the protein specifically binds to polyclonal antibodies to TL- γ . The invention also concerns antibodies to TL- γ , methods for screening biol. active TL- γ , and kits for screening. Using PCR and degenerate primers, TL- γ was amplified from Thermomyces lanuginosus genomic DNA. The nucleic acid sequence was then used as a probe to isolate a longer TL- γ sequence. Recombinant TL- γ was prepared in order to test its activity in a microtubule gliding assay. The

pET23-TL-γ expression vector was constructed and expressed in E. coli. The kinesin TL- γ protein was isolated, it was very stable retaining 100% activity up to 40° after incubation for 15 min as measured using a microtubule dependent ATPase assay. Freshly prepared protein was used to assay microtubule gliding activity. Taxol stabilized microtubule seeds brightly labeled with rhodamine were prepared by incubating a 1:1 ratio of rhodamine labeled bovine brain tubulin; also unlabeled bovine brain tubulin was incorporated into the assay. Flow chambers prepared were preadsorbed with TL- γ motor protein. A microtubule/ATP mix containing polarity marked microtubules, taxol, MgATP and an oxygen scavenging system was then flowed into the chamber. Movement of microtubules was monitored at room temperature on a fluorescence microscope fitted with oil immersion objective and a CCD. For $TL-\gamma$ activity measurement, recombinant TL-γ protein was attached to a glass coverslip using non-specific adhesion, and gliding of polarity marked microtubules containing brightly fluorescent rhodamine labeled seeds near their minus ends was recorded by time-lapse digital fluorescence microscopy. Microtubules moved with brightly fluorescent seeds leading, indicating that the immobilized TL-y protein was moving toward microtubule plus ends. No movement was observed in the absence of TL- γ . This experiment demonstrates that TL- γ has plus-ended microtubule motor activity.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 1999:451195 CAPLUS

DOCUMENT NUMBER: 131:97592

TITLE: Kinesin motor modulators derived from the marine

sponge adocia

INVENTOR(S): Goldstein, Lawrence S. B.; Faulkner, David

John; Sakowicz, Roman; Berdelis, Michael S.; Blackburn, Christine L.; Hopmann, Cordula

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 73 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Facelite English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PA	rent :	NO.			KIN)	DATE			APPL	ICAT:	ION I	. OI		D	ATE	
WO	9934	806			A1	-	1999	0715	,	WO 1:	999-1	US32:	1		1	9990:	106
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		ΚE,	KG,	ΚP,	KR,	KZ,	LC,	LK,	LR,	LS,	LT,	LU,	LV,	MD,	MG,	MK,	MN,
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		TR,	TT,	UA,	UG,	US,	UZ,	VN,	YU,	ZW,	AM,	ΑZ,	BY,	KG,	ΚZ,	MD,	RU,
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US	6207	403			· B1		2001	0327	1	US 1:	999-:	2267	72		1	9990	106
JР	2002	5001	90		T2		2002	0108	,	JP 2	000-!	5272	55		1	9990	106
US	6489	134			B1		2002	1203	1	US 2	000-	7246	09		2	0001	128

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US 2003127621
                                20030710
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                                20040817
                          B2
     US 2004176625
                         A1
                                20040909
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PRIORITY APPLN. INFO.:
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                                                                A3 19990106
                                            US 1999-226772
                                                                W 19990106
                                            WO 1999-US321
                                                                A1 20001128
                                            US 2000-724609
                                            US 2002-305857
                                                                A1 20021127
```

OTHER SOURCE(S): MARPAT 131:97592

ED Entered STN: 23 Jul 1999

AB This invention provides novel compds. derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compds. act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications [e.g. in mitigating a variety of pathol. conditions characterized by abnormal cell mitosis].

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 1999:194248 CAPLUS

DOCUMENT NUMBER: 130:233824

TITLE: Plus end-directed microtubule motor protein CENP-E

required for Xenopus chromosome congression

INVENTOR(S): Wood, Kenneth W.; Sakowicz, Roman;

Goldstein, Lawrence S. B.; Cleveland, Don W.

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

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WO	9913										1998-					9980	910
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	RW:	GH,	GM,	ΚE,	LS,	MW,	SD,	SZ,	UG,	ZW	, AT,	BE,	CH,	CY,	DE,	DK,	ES,
		FI,	FR,	GB,	GR,	ΙE,	ΙT,	LU,	MC,	NL	, PT,	SE,	BF,	ВJ,	CF,	CG,	CI,
		CM,	GΑ,	GN,	GW,	ML,	MR,	ΝE,	SN,	TD	, TG						
CA	2303	484			AA		1999	0318		CA	1998-	2303	484		1	9980	910
AU	9893	918			A1		1999	0329		AU :	1998-	9391	8		1	9980	910
AU	7453	85			B2		2002	0321									
EP	1012	249			A1		2000	0628		EP	1998-	9470	39		1	9980	910
	R:	ΑT,	BE,	CH,	DE,	DK,	ES,	FR,	GB,	GR	, IT,	ĿΙ,	LU,	NL,	SE,	MC,	PT,
		ΙE,	FI														
JP	2001	5268	81		T2		2001	1225		JP :	2000-	5108	50		1	.9980	910
US	6645	748			В1		2003	1111		US	1998-	1508	67		1	9980	910
US	7009	043			В1		2006	0307		US :	2000-	7245	84		2	0001	128
US	2005	1916	31		A1		2005	0901		US :	2003-	6502	80		2	0030	827
PRIORIT	Y APP	LN.	INFO	. :						US	1997-	5864	5P		P 1	9970	911
										US	1998-	1508	67		A1 1	9980	910
							•			WO	1998-	US19	231	1	W 1	9980	910

ED Entered STN: 25 Mar 1999

AB The invention provides isolated nucleic acid and amino acid sequences of

Xenopus centromere-associated protein-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biol. active CENP-E, and kits for screening for CENP-E modulators. The full-length cDNA sequences of XCENP-E encodes a protein of 2954 amino acids with a predicted mol. mass of 340 kDa. XCENP-E is a member of the kinesin superfamily of motor proteins, and consists of a 500-amino acid globular N-terminal domain containing a kinesin-like microtubule motor domain linked to a globular tail domain by a region predicted to form a long, discontinuous α -helical coiled coil. The is the first biol. active CENP-E isolated and, surprisingly and contrary to previous reports, it demonstrates a motor that powers chromosome movement toward microtubule plus ends. Using immunodepletion and antibody addition to Xenopus egg exts., the present invention further demonstrates that CENP-E plays an essential role in congression.

REFERENCE COUNT: THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4

ACCESSION NUMBER:

1999:420033 CAPLUS

DOCUMENT NUMBER:

131:211782

TITLE:

Adociasulfates 1-6, inhibitors of kinesin motor

proteins from the sponge Haliclona (aka Adocia) sp.

AUTHOR (S):

Blackburn, Christine L.; Hopmann, Cordula;

Sakowicz, Roman; Berdelis, Michael S.;

CORPORATE SOURCE:

Goldstein, Lawrence S. B.; Faulkner, D. John Scripps Institution of Oceanography, University of

California at San Diego, La Jolla, CA, 92093-0212, USA Journal of Organic Chemistry (1999), 64(15), 5565-5570

SOURCE:

CODEN: JOCEAH; ISSN: 0022-3263

PUBLISHER:

American Chemical Society

DOCUMENT TYPE:

Journal English

LANGUAGE: Entered STN: 08 Jul 1999

GI

* STRUCTURE DIAGRAM TOO LARGE FOR DISPLAY - AVAILABLE VIA OFFLINE PRINT *

Adociasulfates 1-6 were isolated from an extract of the Palauan sponge Haliclona (aka Adocia) sp. that inhibited the transport of stabilized microtubules by the motor protein kinesin, which was immobilized on a microscope slide. The structures of adociasulfates 1-6, the relative stereochem. of adociasulfates 1 (I), 2, 5, and 6, and the relative stereochem. of subunits of adociasulfates 3 (II) and 4 were determined by interpretation of spectroscopic data. In a quant. assay that measures ATP hydrolysis by kinesin, adociasulfates 2 and 6 were the most active. 7

REFERENCE COUNT:

THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 10

ACCESSION NUMBER:

1996:282241 CAPLUS

DOCUMENT NUMBER: TITLE:

124:310323 The muscle in kinesin

AUTHOR(S):

Sakowicz, Roman; Goldstein, Lawrence S.

CORPORATE SOURCE:

Howard Hughes Medical Inst., Univ. California, La

Jolla, CA, 92093-0683, USA

SOURCE:

Nature Structural Biology (1996), 3(5), 404-407

Hines 09/235416 Page 12

CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER: Nature Publishing Co.
DOCUMENT TYPE: Journal; General Review

LANGUAGE: English ED Entered STN: 14 May 1996

AB A review, with 41 refs. The first high resolution structures of the kinesin

and NCD motor proteins reveal their surprising similarity to myosin but

leave open the tantalizing question of what properties eet. the

directionality of movement along microtubules.

L140 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11

ACCESSION NUMBER: 1997:151799 CAPLUS

DOCUMENT NUMBER: 126:234999

TITLE: Single molecules solvated in pores of polyacrylamide

gels

AUTHOR(S): Dickson, Robert M.; Norris, D. J.; Tzeng, Yih-Ling;

Sakowicz, R.; Goldstein, L. S. B.;

Moerner, W. E.

CORPORATE SOURCE: Department Chemistry Biochemistry, University

California San Diego, La Jolla, CA, 92093-0340, USA Molecular Crystals and Liquid Crystals Science and

Technology, Section A: Molecular Crystals and Liquid

Crystals (1996), 291, 31-39 CODEN: MCLCE9; ISSN: 1058-725X

PUBLISHER: Gordon & Breach

DOCUMENT TYPE: Journal LANGUAGE: English ED Entered STN: 08 Mar 1997

SOURCE:

AB Individual fluorescent mols. and individual singly-labeled proteins have been observed in the water-filled pores of poly(acrylamide) gels with far-field microscopy. The mol. range of motion is dramatically reduced by the gel framework, thus allowing single mols. to be studied in an aqueous environment for long periods of time. For the small fluorophores, the gel restricts Brownian motion by approx. two orders of magnitude in each direction, thus greatly enhancing the mol.'s detectability. In contrast to dry polymeric hosts, the gel is composed primarily of water and the majority of mols. remain in solution, thus making these gels an ideal medium in which to utilize single mol. detection methods for the study of biol. systems in vitro.

L140 ANSWER 11 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN DUPLICATE 6

ACCESSION NUMBER: 1999:185585 BIOSIS DOCUMENT NUMBER: PREV199900185585

TITLE: Single-molecule studies of fluorescent proteins and

enzymes.

AUTHOR(S): Moerner, W. E. [Reprint author]; Peterman, E. J.; Sosa, H.;

Brasselet, S.; Dickson, R. M.; Kummer, S.; Sakowicz,

R.; Goldstein, L. S. B.

CORPORATE SOURCE: Department of Chemistry, Stanford University, Stanford, CA,

USA

SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2,

pp. A20. print.

Meeting Info.: Forty-third Annual Meeting of the

Biophysical Society. Baltimore, Maryland, USA. February

13-17, 1999.

CODEN: BIOJAU. ISSN: 0006-3495.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

Hines 39/235416 . Page 13

ENTRY DATE: Entered STN: 5 May 1999

Last Updated on STN: 5 May 1999

ED Entered STN: 5 May 1999

Last Updated on STN: 5 May 1999

L140 ANSWER 12 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN DUPLICATE 8

ACCESSION NUMBER: 1999:15470 BIOSIS DOCUMENT NUMBER: PREV199900015470

TITLE: Study of the orientation of kinesin motors bound to

microtubules using single molecule fluorescence

polarization spectroscopy.

AUTHOR(S): Sosa, H. [Reprint author]; Peterman, E. J. G.; Dickson, R.

M.; Sakowicz, R.; Moerner, W. E.; Goldstein,

L. G

CORPORATE SOURCE: Dep. Pharmacology, Univ. Calif., San Diego, CA 92093, USA

SOURCE: Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No.

SUPPL., pp. 28A. print.

Meeting Info.: 38th Annual Meeting of the American Society for Cell Biology. San Francisco, California, USA. December

12-16, 1998. American Society for Cell Biology.

CODEN: MBCEEV. ISSN: 1059-1524.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 20 Jan 1999

Last Updated on STN: 20 Jan 1999

ED Entered STN: 20 Jan 1999

Last Updated on STN: 20 Jan 1999

L140 ANSWER 13 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER: 2006:342933 BIOSIS DOCUMENT NUMBER: PREV200600349154

TITLE: Plus end-directed microtubule motor required for chromosome

congression.

AUTHOR(S): Wood, Kenneth W. [Inventor]; Sakowicz, Roman

[Inventor]; Goldstein, Lawrence S. B. [Inventor];

Cleveland, Don W. [Inventor]

CORPORATE SOURCE: Foster City, CA USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 07009043 20060307

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (MAR 7 2006) CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent

LANGUAGE: Facence English

ENTRY DATE: Entered STN: 12 Jul 2006

Last Updated on STN: 12 Jul 2006

ED Entered STN: 12 Jul 2006

Last Updated on STN: 12 Jul 2006

AB The invention provides isolated nucleic acid and amino acid sequences of Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biologically active CENP-E, and kits for screening for CENP-E modulators.

L140 ANSWER 14 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER: 2004:468880 BIOSIS DOCUMENT NUMBER: PREV200400473914

Hines 09/235416 Page 14

TITLE: Identification and expression of a novel kinesin motor

protein.

AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author];

Goldstein, Lawrence S. B. [Inventor]

CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6815169 20041109

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Nov 9 2004) Vol. 1288, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file.

ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent LANGUAGE: English

ENTRY DATE: Entered STN: 9 Dec 2004

Last Updated on STN: 9 Dec 2004

ED Entered STN: 9 Dec 2004

Last Updated on STN: 9 Dec 2004

AB The invention provides isolated nucleic acid and amino acid sequences of

TL-gamma, antibodies to TL-gamma,

methods of screening for ${\bf TL}\text{-}{\bf gamma}$ modulators using biologically active ${\bf TL}\text{-}{\bf gamma}$, and kits for screening

for TL-gamma modulators.

L140 ANSWER 15 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN .

ACCESSION NUMBER: 2004:376082 BIOSIS DOCUMENT NUMBER: PREV200400381987

TITLE: Kinesin motor modulators derived from the marine sponge

Adocia.

AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint

Author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula

[Inventor]

CORPORATE SOURCE: Frankfurt am Main, Germany

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6777200 20040817

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Aug 17 2004) Vol. 1285, No. 3. http://www.uspto.gov/web/menu/patdata.html. e-file.

ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent LANGUAGE: English

ENTRY DATE: Entered STN: 22 Sep 2004

Last Updated on STN: 22 Sep 2004

ED Entered STN: 22 Sep 2004

Last Updated on STN: 22 Sep 2004

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 16 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

ACCESSION NUMBER: 2004:332625 BIOSIS DOCUMENT NUMBER: PREV200400337426

TITLE: Thermomyces lanuginosus kinesin motor protein and methods

of screening for modulators of kinesin proteins.

AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author];

Goldstein, Lawrence S. B. [Inventor]

Hines 09/235416 Page: 15

CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6764830 20040720

Official Gazette of the United States Patent and Trademark SOURCE:

> Office Patents, (July 20 2004) Vol. 1284, No. 3. http://www.uspto.gov/web/menu/patdata.html. e-file.

ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE:

Patent English

LANGUAGE: ENTRY DATE:

Entered STN: 4 Aug 2004

Last Updated on STN: 4 Aug 2004

Entered STN: 4 Aug 2004

Last Updated on STN: 4 Aug 2004

The invention provides isolated nucleic acid and amino acid sequences of AB

TL-gamma, antibodies to TL-gamma,

methods of screening for TL-gamma modulating using biologically active TL-gamma, and kits for screening

for TL-gamma modulators.

L140 ANSWER 17 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER:

2004:7637 BIOSIS

DOCUMENT NUMBER:

PREV200400008401

TITLE:

Plus end-directed microtubule motor required for chromosome

congression.

AUTHOR (S):

Wood, Kenneth W. [Inventor, Reprint Author]; Sakowicz,

Roman [Inventor]; Goldstein, Lawrence S. B. [Inventor]; Cleveland, Don W. [Inventor]

CORPORATE SOURCE:

Delmar, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6645748 20031111

SOURCE:

Official Gazette of the United States Patent and Trademark

Office Patents, (Nov 11 2003) Vol. 1276, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file.

ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE:

Patent

LANGUAGE: ENTRY DATE: English Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

The invention provides isolated nucleic acid and amino acid sequences of AB Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biologically active CENP-E, and kits for screening

for CENP-E modulators.

L140 ANSWER 18 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

ACCESSION NUMBER:

2003:56963 BIOSIS

DOCUMENT NUMBER:

PREV200300056963

TITLE:

Kinesin motor modulators derived from the marine sponge

Adocia.

AUTHOR (S):

Goldstein, Lawrence S.B. [Inventor, Reprint

Author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula

[Inventor]

CORPORATE SOURCE:

San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6489134 20021203

SOURCE:

Official Gazette of the United States Patent and Trademark

Hines 09/235416 Page 16

Office Patents, (Dec 3 2002) Vol. 1265, No. 1. http://www.uspto.gov/web/menu/patdata.html. e-file.

ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent LANGUAGE: English

ENTRY DATE: Entered STN: 22 Jan 2003

Last Updated on STN: 22 Jan 2003

ED Entered STN: 22 Jan 2003

Last Updated on STN: 22 Jan 2003

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 19 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER: 2001:461909 BIOSIS DOCUMENT NUMBER: PREV200100461909

TITLE: Kinesin motor modulators derived from the marine sponge

Adocia.

AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint

author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula

[Inventor]

CORPORATE SOURCE: San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6207403 20010327

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Mar. 27, 2001) Vol. 1244, No. 4. e-file.

CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent LANGUAGE: English

ENTRY DATE: Entered STN: 3 Oct 2001

Last Updated on STN: 22 Feb 2002

ED Entered STN: 3 Oct 2001

Last Updated on STN: 22 Feb 2002

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 20 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER: 1998:20152 BIOSIS DOCUMENT NUMBER: PREV199800020152

TITLE: CENP-E is a plus end-directed kinetochore motor required

for chromosome congression.

AUTHOR(S): Wood, K. W. [Reprint author]; Sakowicz, R.;

Goldstein, L. S. B.; Cleveland, D. W. [Reprint

author]

CORPORATE SOURCE: Lab. Cell Biol., Ludwig Inst. Cancer Research, La Jolla, CA

92093-0660, USA

SOURCE: Molecular Biology of the Cell, (Nov., 1997) Vol. 8, No.

SUPPL., pp. 125A. print.

Meeting Info.: 37th Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 13-17,

1997. American Society for Cell Biology.

CODEN: MBCEEV. ISSN: 1059-1524.

DOCUMENT TYPE:

Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE:

English

ENTRY DATE:

Entered STN: 5 Jan 1998

Last Updated on STN: 5 Jan 1998

Entered STN: 5 Jan 1998

Last Updated on STN: 5 Jan 1998

L140 ANSWER 21 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on

ACCESSION NUMBER:

1997:95559 BIOSIS

DOCUMENT NUMBER:

PREV199799394762

TITLE:

Cloning, expression, and purification of kinesin superfamily members from the thermophilic fungus.

AUTHOR (S):

Sakowicz, R.; Farlow, S.; Goldstein, L. S.

CORPORATE SOURCE:

Howard Hughes Med. Inst., Div. Cell. Mol. Med., Dep. Pharmacol., Univ. Calif. San Diego, 9500 Gilman Dr., La

Jolla, CA 92093-0683, USA

SOURCE:

Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL.,

pp. 215A.

Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology. San Francisco, California, USA. December

7-11, 1996.

CODEN: MBCEEV. ISSN: 1059-1524.

DOCUMENT TYPE:

Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

Conference; (Meeting Poster)

LANGUAGE:

English ENTRY DATE:

Entered STN: 3 Mar 1997

Last Updated on STN: 3 Mar 1997

ED Entered STN: 3 Mar 1997

Last Updated on STN: 3 Mar 1997

L140 ANSWER 22 OF 26 LIFESCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER:

2003:77194 LIFESCI

TITLE:

Kinesin motor modulators derived from the marine sponge

Adocia

AUTHOR:

Goldstein, L.S.B.; Faulkner, D.J.; Sakowicz,

R.; Berdelis, M.S.; Blackburn, C.L.; Hopmann, C.

CORPORATE SOURCE:

The Regents of the University of California, Oakland,

California

SOURCE:

(20021203) . US Patent: 6489134; US CLASS: 435/21; 435/6;

514/172; 514/182; 514/518; 585/350.

DOCUMENT TYPE:

Patent

FILE SEGMENT: LANGUAGE:

04

vitro and in vivo applications.

English

SUMMARY LANGUAGE:

English

This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulat kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in

L140 ANSWER 23 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER:

1999:35078 CONFSCI

DOCUMENT NUMBER:

99-047572

TITLE:

Single-molecule studies of fluorescent proteins and

enzymes. Topic(s): 09A 01D

AUTHOR: Moerner, W.E.; Peterman, E.J.; Sosa, H.; Brasselet, S.;

Dickson, R.M.; Kummer, S.; Sakowicz, R.;

Goldstein, L.S.B.

CORPORATE SOURCE: Stanford Univ., USA

SOURCE: Biophysical Society, 9650 Rockville Pike, Bethesda, MD

20814, USA; phone: (301) 530-7114; fax: (301) 530-7133;

email: society@biophysics.faseb.org; URL:

www.biophysics.faseb.org, Abstracts available. Price \$25...

Meeting Info.: 991 0048: 43rd Annual Meeting of the

Biophysical Society (9910048). Baltimore, MD (USA). 13-17

Feb 1999. Biophysical Society.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

DCCP

LANGUAGE:

English

L140 ANSWER 24 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER:

1999:26143 CONFSCI

DOCUMENT NUMBER:

99-038637

TITLE:

Study of the orientation of kinesin motors bound to

microtubules using single molecule fluorescence

polarization spectroscopy

AUTHOR:

Sosa, H.; Peterman, E.J.G.; Dickson, R.M.; Sakowicz,

R.; Moerner, W.E.; Goldstein, L.G.

CORPORATE SOURCE:

Dep. Pharmacol., Univ. California at San Diego, CA 92093,

IICA

SOURCE:

American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814, USA; phone: (301) 530-7153; fax: (301)

530-7139; email: ascbinfo@ascb.org; URL:

www.ascb.org/ascb/, Abstracts available. Price \$45. Paper

No. 159.

Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance, Mark-Rambar Family

Foundation.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

DCCP

LANGUAGE:

English

L140 ANSWER 25 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on

STN

ACCESSION NUMBER: 1997:848661 SCISEARCH

THE GENUINE ARTICLE: YF096

TITLE:

CENP-E is a plus end-directed kinetochore motor required

for chromosome congression

AUTHOR:

Wood K W (Reprint); Sakowicz R; Goldstein L

S B; Cleveland D W

CORPORATE SOURCE:

UNIV CALIF SAN DIEGO, CELL BIOL LAB, LUDWIG INST CANC RES, LA JOLLA, CA 92093; UNIV CALIF SAN DIEGO, HOWARD HUGHES

MED INST, DIV CELLULAR & MOL MED, LA JOLLA, CA 92093

COUNTRY OF AUTHOR: U

SOURCE:

MOLECULAR BIOLOGY OF THE CELL, (NOV 1997) Vol. 8, Supp.

[S], pp. 723-723. ISSN: 1059-1524.

PUBLISHER:

AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750,

BETHESDA, MD 20814-2755 USA.

DOCUMENT TYPE:

Conference; Journal

LANGUAGE:

English

REFERENCE COUNT:

211

Hines 09/233416 Page 19

ENTRY DATE:

Entered STN: 1997

Last Updated on STN: 1997

Entered STN: 1997

Last Updated on STN: 1997

L140 ANSWER 26 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on

ACCESSION NUMBER: 1997:46229 SCISEARCH

THE GENUINE ARTICLE: WB018

Cloning, expression, and purification of kinesin TITLE: superfamily members from the thermophilic fungus.

Sakowicz R (Reprint); Farlow S; Goldstein L AUTHOR:

UNIV CALIF SAN DIEGO, DEPT PHARMACOL, DIV CELLULAR & MOL CORPORATE SOURCE:

MED, HOWARD HUGHES MED INST, LA JOLLA, CA 92093

COUNTRY OF AUTHOR:

USA

MOLECULAR BIOLOGY OF THE CELL, (DEC 1996) Vol. 7, Supp. SOURCE:

> [S], pp. 1250-1250. ISSN: 1059-1524.

AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750, PUBLISHER:

BETHESDA, MD 20814-2755 USA.

DOCUMENT TYPE:

Conference; Journal

LANGUAGE:

English

REFERENCE COUNT:

ENTRY DATE: Entered STN: 1997

Last Updated on STN: 1997

Entered STN: 1997

Last Updated on STN: 1997

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L7	1841	EA FILE=CAPLUS ABB=ON KINESINS/CT
L9	20619	EA FILE=CAPLUS ABB=ON MICROTUBULE#/OBI
L10		EA FILE=CAPLUS ABB=ON MOTOR/OBI(L)PROTEIN#/OBI
L11		EA FILE=REGISTRY ABB=ON "PROTEIN KINASE"/CN
L12	97768	EA FILE=CAPLUS ABB=ON L11 OR PROTEIN KINASE#/OBI
L14	1	EA FILE=CAPLUS ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)

=> s 114 not 1139

0 L14 NOT

=> fil wpix; d que 130

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FILE LAST UPDATED: 1 SEP 2006 <20060901/UP>
MOST RECENT DERWENT UPDATE: 200656 <200656/DW>
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1 SEA FILE=WPIX ABB=ON (THERMOMYCES LANUGINOSUS/BI,ABEX OR TL/BI,ABEX) (A) GAMMA/BI,ABEX

=> s 130 not 131

L144

0 L30 NOT (L31) printed

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 171

L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L64 13861 SEA KINESIN#
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#
L66 7756 SEA MOTOR PROTEIN#
L67 2654 SEA END DIRECT?
L70 567385 SEA PROTEIN KINASE#
L71 3 SEA L63 AND (L64 OR L65 OR L66 OR L67 OR L70)

=> s 171 not 168

L145 0 L71 NOT (L68) previously

=> fil medl; d que 189

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

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http://www.nlm.nih.gov/mesh/

http://www.nlm.nih.gov/pubs/techbull/nd04/nd04 mesh.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05 2006 MeSH.html

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MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L82	11	SEA	FILE=MEDLINE	ABB=ON	(THERMOMYCES LANUGINOSUS OR TL) (A) GAMM
		Α			
L84	2094	SEA	FILE=MEDLINE	ABB=ON	KINESIN/CT
L85	17967	SEA	FILE=MEDLINE	ABB=ON	MICROTUBULES/CT
L86	76212	SEA	FILE=MEDLINE	ABB=ON	ENZYME INHIBITORS/CT
L87	1529	SEA	FILE=MEDLINE	ABB=ON	MOTOR PROTEIN#
L88	359	SEA	FILE=MEDLINE	ABB=ON	END DIRECT?
L89	0	SEA	FILE=MEDLINE	ABB=ON	L82 AND (L84 OR L85 OR L86 OR L87 OR
		L881)		

=> fil embase; d que l118

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This file contains CAS Registry Numbers for easy and accurate substance identification.

L109	16 S	SEA FILE=EMBASE ABB=ON	(THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L112 L113 L114 L115	3476 S 754 S	SEA FILE=EMBASE ABB=ON SEA FILE=EMBASE ABB=ON SEA FILE=EMBASE ABB=ON SEA FILE=EMBASE ABB=ON	KINESIN/CT MICROTUBULE ASSEMBLY/CT MICROTUBULE PROTEIN/CT MICROTUBULE/CT
L116 L117	316 S	SEA FILE=EMBASE ABB=ON SEA FILE=EMBASE ABB=ON	END DIRECT? MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L118		SEA FILE=EMBASE ABB=ON OR L116 OR L117)	L109 AND (L112 OR L113 OR L114 OR L115

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=> => => fil capl; d que 118 FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

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L7	1841	SEA	FILE=CAPLUS	ABB=ON	KINESINS/CT
L9	20619	SEA	FILE=CAPLUS	ABB=ON	MICROTUBULE#/OBI
L10	3352	SEA	FILE=CAPLUS	ABB=ON	MOTOR/OBI(L)PROTEIN#/OBI
L15	220	SEA	FILE=CAPLUS	ABB=ON	L7 AND L9 AND L10
L17	48	SEA	FILE=CAPLUS	ABB=ON	END DIRECT?/OBI
L18	3.	SEA	FILE=CAPLUS	ABB=ON	L15 AND L17

=> s 118 not 1139

3 L18 NOT (L139) puriously ed => fil wpix; d que 139; d que 140

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L32	252	SEA FILE=WPIX	ABB=ON	KINESIN#/BI,ABEX
L33	811	SEA FILE=WPIX	ABB=ON	MICROTUBULE#/BI, ABEX OR MICRO TUBULE#/BI,
		ABEX		
L34	120	SEA FILE=WPIX	ABB=ON	MOTOR PROTEIN#/BI,ABEX
L35	1863	SEA FILE=WPIX	ABB=ON	END DIRECT?/BI,ABEX
L39	3	SEA FILE=WPIX	ABB=ON	L32 AND L33 AND L34 AND L35
				•
L32	252	SEA FILE=WPIX	ABB=ON	KINESIN#/BI,ABEX
L33	811	SEA FILE=WPIX	ABB=ON	MICROTUBULE#/BI, ABEX OR MICRO TUBULE#/BI,
		ABEX		•

ABEX
L34
120 SEA FILE=WPIX ABB=ON MOTOR PROTEIN#/BI,ABEX
L35
1863 SEA FILE=WPIX ABB=ON END DIRECT?/BI,ABEX
L36
4006 SEA FILE=WPIX ABB=ON PROTEIN KINASE#/BI,ABEX
L37
105 SEA FILE=WPIX ABB=ON L32 AND (L33 OR L34 OR L35)
L40
1 SEA FILE=WPIX ABB=ON L37 AND L36

=> s 139,140 not 131

L147 3 (L39 OR L40) NOT (L31) printed

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 175

13861 SEA KINESIN# L64

132140 SEA MICROTUBULE# OR MICRO TUBULE# L65

1,66 7756 SEA MOTOR PROTEIN# 2654 SEA END DIRECT? 1.67

20 SEA L64 (5A) L65 (5A) L66 (5A) L67 1.75

=> s 175 not 168

20 L75 NOT (L68) previously inted L148

=> fil medl; d que 192

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http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html

http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

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L84 2094 SEA FILE=MEDLINE ABB=ON KINESIN/CT L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN# L87

L88 L92 359 SEA FILE=MEDLINE ABB=ON END DIRECT?
9 SEA FILE=MEDLINE ABB=ON L87(8A)L88 AND L84 AND L85

=> s 192 not 183

L149

9 L92 NOT (L83) previous

=> fil embase; d que 1119

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L112	2142	SEA FILE=EMBASE ABB=O	N KINESIN/CT
L113	3476	SEA FILE=EMBASE ABB=O	N MICROTUBULE ASSEMBLY/CT
L114	754	SEA FILE=EMBASE ABB=O	N MICROTUBULE PROTEIN/CT
L115	13611	SEA FILE=EMBASE ABB=O	N MICROTUBULE/CT
L116	316	SEA FILE=EMBASE ABB=O	N END DIRECT?
L117	569	SEA FILE=EMBASE ABB=O	N MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L119	7	SEA FILE=EMBASE ABB=O	N L112 AND (L113 OR L114 OR L115) AND

=> s 1119 not 1110

L150

7 L119 NOT (L110) previously printed

=> => dup rem 1149,1146,1147,1150,1148
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28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED) L151

ANSWERS '1-9' FROM FILE MEDLINE ANSWERS '10-12' FROM FILE CAPLUS ANSWERS '13-15' FROM FILE WPIX ANSWERS '16-21' FROM FILE EMBASE ANSWERS '22-23' FROM FILE BIOTECHNO ANSWERS '24-27' FROM FILE BIOSIS ANSWER '28' FROM FILE LIFESCI

=> d iall 1-9; d ibib ed abs hitind 10-12; d iall abeq tech 13-15; d iall 16-28

L151 ANSWER 1 OF 28 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 2005237850 MEDLINE DOCUMENT NUMBER: PubMed ID: 15875026

The bipolar mitotic kinesin Eq5 moves on both microtubules TITLE:

that it crosslinks.

Kapitein Lukas C; Peterman Erwin J G; Kwok Benjamin H; Kim AUTHOR:

Jeffrey H; Kapoor Tarun M; Schmidt Christoph F

CORPORATE SOURCE: Department of Physics and Astronomy and Laser Centre, Vrije

Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The

Netherlands.

Nature, (2005 May 5) Vol. 435, No. 7038, pp. 114-8. SOURCE:

Journal code: 0410462. E-ISSN: 1476-4687.

England: United Kingdom PUB. COUNTRY:

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

English LANGUAGE:

Priority Journals FILE SEGMENT:

200505 ENTRY MONTH:

Entered STN: 6 May 2005 ENTRY DATE:

Last Updated on STN: 19 May 2005 Entered Medline: 18 May 2005

ABSTRACT:

During cell division, mitotic spindles are assembled by microtubule-based motor proteins. The bipolar organization of spindles is essential for proper segregation of chromosomes, and requires plus-end-directed

homotetrameric motor proteins of the widely conserved kinesin-5 (BimC) family. Hypotheses for bipolar spindle formation include the 'push-pull mitotic muscle' model, in which kinesin-5 and opposing motor proteins act between overlapping microtubules. However, the precise roles of kinesin-5 during this process are unknown. Here we show that the vertebrate kinesin-5 Eg5 drives the sliding of microtubules depending on their relative orientation. We found in controlled in vitro assays that Eg5 has the remarkable capability of simultaneously moving at approximately 20 nm s(-1) towards the plus-ends of each of the two microtubules it crosslinks. For anti-parallel microtubules, this results in relative sliding at approximately 40 nm s(-1), comparable to spindle pole separation rates in vivo. Furthermore, we found that Eg5 can tether microtubule plus-ends, suggesting an additional

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Huntington's

TL-gamma; kinesin; motor protein; microtubule; unc-104; infection; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;

disease; amyotrophic lateral sclerosis.

Thermomyces lanuginosus kinesin motor protein TL-gamma

26-0CT-1999 AAY06618;

(first

entry)

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Aab63189 Gene 5 hu	Adj94856 Novel NOV	Human	Human	_	Novel	-	Human	Aed07567 Chromosom	Human	Adm04401 Human pro	Adr66053 Human pro	Adr66951 Human pro	Adr66054 Human pro		Abb62962 Drosophil	Mouse	Adl83235 Human PRO	Adj69671 Human hea	Human	Human	Abp51294 Human MDD

ALIGNMENTS

AAY06618 RESULT 1

AAY06618 standard; protein;

784

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WPI; 1999-493950/41. N-PSDB; AAX87656. Sakowicz R, 23-JAN-1998; 22-JAN-1999; 29-JUL-1999 W09937659-A1 Thermomyces lanuginosus. (REGC) UNIV CALIFORNIA. Goldstein LSB; 98US-0072361P. 99WO-US001355

New nucleic acid encoding microtubule motor protein, used for diagnosis of fungal infection and neurodegenerative disease.

Claim 5; Page 70-71; 75pp; English.

This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family and kinesin superfamily. The invention provides TL-gamma nucleic acids (see AAX87656), proteins and antibodies, and methods of screening for TL-gamma modulators potentially useful for treating hyphal fungal infections and diseases caused by mutated TL-gamma, e.g. neurodegeneration involving anterograde axonal transport, such as Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral sclerosis. Detection of TL-gamma allows differentiation between hyphal non-hyphal fungal infections

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RESULT 2
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Best Local Similarity
Matches 784; Conserv
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 Human diagnostic and therapeutic pprotein SEQ ID NO:3897.
                                                      ABM83648;
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100.0%; Pred. No. 6.5e-299;
tive 0; Mismatches 0;
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gene
therapy; human diagnostic and
  therapeutic polynucleotide; dithp
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12-SEP-2003; 2003WO-US028227

Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Hooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au Ap, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, W MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ; 12-SEP-2002; 12-SEP-2002; INCYTE CORP 2002US-0410259P 2002US-0410260P

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o in gene mapping. õ

2004-329368/30. DB; ACN42300.

Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, or disorder, neurological disorders, gastrointestinal disorder, or CI infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC polymorphisms, as molecular weight markers, and for somatic or germline CC polymorphisms, as molecular sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 1714 AA;

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                                                 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV
                                                               YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLBIYNERVRDLLNPSTKGNLKV
                                                                                                                        FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                                                                                           GASVKVAVRVRPENSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS
                                                                                                                                                                               GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGABEKARKSGKTIMDGPKAFA 63
REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK
                                                                                                     FDYSYWS--HTSPEDINYASOKOVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTWMG
                                                                                                                                                                                                               Conservative
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%; Pred. No. 6.4e-119;
127; Mismatches 174;
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RRESULT 3
ABM83647
ID ABM8
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XX ABM8
XX ABM8
DT 18-N
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                                                   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder IV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Stevens CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze Patury S, Shi X, Suarez CJ;
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   WPI; 2004-329368/30
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12-SEP-2002; 2002US-0410260P
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                                                                                                               Kirton ES;
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N-PSDB; ACN42299

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o in gene mapping.

Claim Page; 190pp; English

The invention relates to novel diagnostic and therapeutic polynucleotides considered from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human considered to diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, or autoimmune/inflammatory disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp consciutes may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 1721 AA;

Matches Query Match Best Local

358; Conservative

127;

Mismatches

Indels Length 1721

Gaps

16;

Similarity

41.8%; Score 1684.5; DB 46.5%; Pred. No. 6.5e-119

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VVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQSLLRHS
                             LVNLNEDPLMSECLLYYIKDGITRVGREDGERRQDIVLSGHFIKEEHCVFRSDSRGGSEA
                                                                                              IERLKSTEKIIAELNETWEEKLRRTEAIRMEREALLAEMGVAMREDGGTLGVFSPKKTPH
                                                                                                                VEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPH
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            The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, autoimmune/inflammatory disorders, developmental disorder, endocrine autoimmune/inflammatory disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fund or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the convention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly cc from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietz Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                    Claim 27; Page; 190pp; English
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N-PSDB; ACN42323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385;
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MKDEEIKVLRNKMLKMEKVL 904
                                                                                                                                                         RLSKDSKWVTISDLKIQAVKEICYEVA-LNDFRHSRQEIEALAIVKMKELCAMYGKKDPN
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                                     ASNVDVEELRQQQAQMEEAL
                                                                            E-RDSWRAV-ARDVWDTVGVGDEKIEDVMATGKGSTDVDDLKVHIDKLEDILQEVKKQNN
                                                                                                                EDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDD-----DGDALFFGDKKSKQD
                                                                                                                                                                                               --GKDSDWFYARREAASAILGLDQKISHLTD-----DELDALFDDVQKARAVRRGLVEDN
                                                                                                                                                                                                                                      DSDSGDDSDKRSCEESWKLITSLREKLPPSKLQTIVKKCGLPSSGKKREPIKMYQIPQRR
                                                                                                                                                                                                                                                                              DGDSRSDS-----
                                                                                                                                                                                                                                                                                                                     PSAETPSEPVDWTFAQRELLEKQGIDMKQEMEKRLQEMEILYKKEKEEADLLLEQQRLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH 489
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41.8%; Pred. No. 9.8e-119;
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Best Local S
Matches 356
                                                                                                                                                                                                     used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietz Patury S, Shi X, Suarez CJ;
                                                                                                                                                                               Sequence 1696 AA;
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
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                                                                                                                                    Local Similarity
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                       FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                    GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                                                                    Conservative
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                                                                                                                                  41.68;
                                                                                                                  128;
                                                                                                                                  Score 1674.5;
Pred. No. 3.76
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Schmidt JP,
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Wright RJ, Bruns CM, Marjanovic MM, Shen F; TA, Suchorolski MT, Altus CM, Pitts SJ, Elde Delegeane AM, Panesar IS, Banville SC, Reddy
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The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, or conditions caused by virus, bacteria, fungion parasite. The dithp CC infections caused by virus, bacteria, fungion parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide conditions, as molecular weight markers, and for somatic or germline conformation. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from the present of the was obtained in electronic format directly from the present of the was obtained in electronic format directly from the present of the was obtained in electronic format directly from the present of the condition of the present of the condition of the present of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condit
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Kwong M, Policky JL,
S, Shi X, Suarez CJ;
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Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve I
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kii
M, Policky JL, Hurwitz BL, Ma Y, Jackson JL,
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Pred. No. 3.7e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                 Stevens KA,
Peralta CH,
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorders, proliferative disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals
                                                                                                                                                                                                                                                                                                                                                                   Lagace RE,
Xu Y, Kwon
                                                                                                                                                                                  Claim 27; Page; 190pp;
                                                                                                                                                                                                                                  molecules, e.g. autoimmune
                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt JP,
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12-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; human diagnostic and therapeutic
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                                                                                                                                                                                                                                 w diagnostic and therapeutic polynucleotides and polypeptides, useful
diagnosing a condition, disease or disorder associated with human
lecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
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DB; ACN42298.
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                                                                                                                                                                                                                                                                                                                                                  RE, Spiro PA, Stewar
Kwong M, Policky JL,
S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                   Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Anderson SB, Stewart EA, Wingrove J, Vitt UA, Kirton ES
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES
Spiro PA, Stewart EA, Ma Y, Jackson JL, Gietz
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2002US-0410260P.
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Best Local
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                                ABM83650;
                                                               ABM83650 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1722 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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(first entry)
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Pred. No. 3.8e-118;
8; Mismatches 175;
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Peralta CH, Anderson SB,
Peralta CH, Anderson SB,
Serace RE, Spiro PA, St
Serace RE, Spiro PA, St
                                                                                                                                                                                                                                          N-PSDB; ACN42302
                                                                                                                                                                                                                                                                                                                   Mooney EM,
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12-SEP-2002; 2002US-0410260P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human diagnostic and therapeutic pprotein SEQ ID NO:3899
                                                                                                                                                                                                                                                                                                                          Harthshorne TA,
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                                                                                                                                                                                                                                                                                        Kirton ES;
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New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or Ħ mapping.

Claim 27; Page; 190pp; English

CC The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A copolynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorders, developmental disorder, or compared to disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp completes may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 1708 AA;

Similarity

41.5%;

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                               KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV
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                                                                                                               FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
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REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
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Pred. No. 4.9e-118;
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            Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegaene AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer Patury S, Shi X, Suarez CJ;
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New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
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with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated Claim 27; Page; 190pp; English

41.4%; Score 1669.5; DB 8 46.8%; Pred. No. 8.9e-118; tive 125; Mismatches 166; в ;-Indels Length 109; Gaps

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KPGQTRVGNVNQDTQAEIRLNGSKILKEHCTFEN----VDNVVTIVPNEKAAVMVNGVR
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                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 356; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIF1A and KIF1B proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease diagnosis and population studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated or purified human kinesin-like protein polynucleotide used to detect HKLP polynucleotides a contiguous span of at least 12 nucleotides.
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                                                                                                                                                                                                                                                                                                                                  Sequence 1816 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 46; Page 189-192; 199pp;
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antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; noctropis neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatica; antiipemic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; hypertension; atherosclerosis; neurodegenerative disorder; hypertension; atherosclerosis; neurodegenerative disorder; asthma; disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; hematopoietic disorder; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation; cell proliferation; hematopoietis; wound healing; angiogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDSDSQSSFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHVFRFNHPEQARAEREK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DNVVTTVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEEARAERQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKKTPHLVNLNEDPLMSECLLYYIKDGITRVGQADAERRQDIVLSGAHIKEEHCIFRSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGGEEATERLKESEKTTAELNETWEEKLRKTEATRMEREALLAEMGVATREDGGTLGVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKQIKCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKRIKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG------GGAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IVSIQQPDATVKK
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17-UIL-2002;
06-AUG-2002;
07-AUG-2002;
07-AUG-2002;
15-AUG-2002;
20-AUG-2002;
23-AUG-2002;
23-AUG-2002;
23-AUG-2002;
23-AUG-2002;
23-AUG-2002;
23-AUG-2002;
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20 NOV-2001

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28 NOV-2001

28 NOV-2001

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04 PEB-2002

04 PEB-2002

05 NAR-2002

27 FEB-2002

27 FEB-2002

13 NAR-2002

                                                        COI CE,
                                                                                              Chaudhuri A,
Gangolli EA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome mapping; tissue typing; pharmacogenomic.
                   Rothenberg ME, Shenoy
Vernet CAM, Zerhusen
                                                                                                                                    Agee ML,
                                 AL, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS uuri A, Dipippo VA, Edinger SR, Eisen A, Ellerman K; Lili EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV; Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I B, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK; berg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ;
                                                                                                                                                                          CURAGEN CORP.
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2001US-031643P

2001US-033164P

2001US-033341P

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2001US-033491P

2001US-0334526P

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2001US-033839P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel isolated polypeptides, mature forms of CC these, or a sequence that is at least 95 % identical to, or having one or CC more conservative amino acid substitutions in the polypeptides. The CC manufacture of a medicament for treating a syndrome associated with a CC muman disease, preferably a NOVX-associated disorder. The nucleic acid molecules polypeptides and antibodies are useful for treating, concerning or diagnosing diseases such metabolic disorders, diabetes, cobsestly, infectious diseases (viral, bacterial, fungal, helminthic, and CC preventing or diagnosing diseases such metabolic disorders, diabetes, cobsestly, infectious diseases (viral, bacterial, fungal, helminthic, and cc protozoal) anorexia, cancer, cardiovascular diseases (hypertension, cc atherosclerosis), neurodegenerative disorders, Alzheimer's disease, parkinson's disease, epilepsy, immune disorders, sathma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as cargets for the identification of small molecules that modulate or cinhbit e.g. neurogenesis, cell differentiation, cell proliferation, cc pensatopoiesis, wound healing and angiogenesis, in gene therapy, in cc pensatopoiesis, wound healing and angiogenesis. The nucleic acids are cf for use in therapeutic or diagnostic methods. The nucleic acids are crossed as hybridization probes, in chromosome mapping, tissue crossored as from a free halony and pharmacogenomics. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim:
Matches 355;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1805 AA;
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)B; ADJ95087.
438 VEQLNOSEKLYRDLNOTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYHSKEMPH
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                                                                                                                                                                                                           KNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGG------GGAGGSGGPVEE----
                                                                                                                                                                                                                                                                                DEETKMDTEK-VAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGNIKVVVRVRDFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                                           KHRYLLASENQRPGHFSTASMGSLTSSPSSCSLSSQVGLTSVTSIQ--ERIMSTPGGEEA
                                                                                                                                  KCNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDVDPLIDDYSGSGSKLKDFQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                         EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
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Pred. No. 1.4e-117;
27; Mismatches 172;
                                                                                              SYPPOTPLEKQ----IVSIQQPDATVKKMSKAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention
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The invention relates to KIFIBb protein which belongs to kinesin superfamily of molecular motor proteins (KIFIB). KIFIBb is useful for screening for a compound binding to it. Composition comprising the selected compound is useful for treating, alleviating, or preventing a kifBlbeta gene-associated disease, in particular Charcot-Marie-Tooth disease type 2A. Transgenic non-human vertebrate, are useful for screening for a candidate compound for treating, alleviating, or preventing a kifIBbeta gene-associated disease. KIFIBb DNA is useful for gene therapy and for recombinant production of polypeptides. KIFIBb and for detecting expression of kifIBbeta gene at the protein level. The present sequence is mouse KIFIBbeta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    agent fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New KIF1Bb polypeptide having motor activity that transports synaptic vesicle precursor, is useful for developing therapeutic or preventive agent for kif1Bb gene-associated diseases e.g. Charcot-Marie-Tooth
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 72-78; 44pp; English.
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disease type 2A;
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47.3%; Pred. No. 1.6e-117;
tive 125; Mismatches 174;
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ABB07867 standard; protein; 1823 ₿

ABB07867;

03-JUL-2002 (first entry)

Human kinesin-associated protein having motor domain

RESULT 13
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MSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGISIEK--GFVGPYH
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                                              DFQNNKHRYLLASENQRPGHFSTASMGSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMST
                                                                                                                                                                      CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR
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                                                                                                          AKQIKCNAVINEGPNAKLVRELKEEVTRLKDLLRAQGLGDIIDIDPLIDDYSGSGSKYLK
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tive 126; Mismatches 173;
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03-AUG-2000;
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Wang Z,
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2000US-00488725.
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J, Zhao
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                                                                                                                  SKAGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDV 688
                                                                                                                                                                               VTEPSILRSGNRIIMGKSHVFRFTHPEQARQERER-----
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N-PSDB; ACN42304.
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Claim 27; Page; 190pp; English

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dikhp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, generative disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 1697 Æ

밁 Ş Query Match Best Local Similarity Matches 350; Conserv GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS Conservative 41.2%; Score 1659.5; 46.7%; Pred. No. 5.2e tive 126; Mismatches .2e-DB 8; Indels Length 107; 1697 Gaps 51 63

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                                                                                                AGSDADGDSRSDSPLPHFRGKDSDWFYARREAASAILGLDQKISHLTDDELDALFDDVQK 690
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Q5AVY3_EMENI
Q4X048_ASPFU
Q5AVY3_EMENI
Q7S784_NEUCR
Q86Z84_BOTCI
Q4HXW9_G1BZE
Q86Z8A_COCHE
Q2UE08_ASPOR
Q4P0W2_USTWA
Q8TG36_USTWA
Q8TG36_USTWA
Q8TG36_HUMAN
Q4VXC3_HUMAN
Q4VXC5_HUMAN
Q4FAL3_MOUSE
Q7PHR1_ANOUSE
Q7PHR1_MOUSE
Q6F5H4_MOUSE
Q4VXC4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
 Q6iuu6 thermomyces
Q4x048 aspergillus
Q5avy3 aspergillus
Q5avy3 aspergillus
Q5avy3 aspergillus
Q8c292 gibberella
Q8c292 gibberella
Q8c294 botrytis ci
Q4hxw9 gibberella
Q8c204 botrytis ci
Q4hxw9 gibberella
Q8c204 ustilago ma
Q8t236 custilago ma
Q8t236 cryptococcu
Q5kng1 cryptococcu
Q5kng1 cryptococcu
Q4vxc3 homo sapien
Q4vycc5 homo sapien
Q4vycc5 homo sapien
Q4vym9 homo sapien
Q4vym9 homo sapien
Q4r9m9 homo sapien
Q4r9m7 homo sapien
Q4r9m7 homo sapien
Q4r9m8 homo sapien
Q4r9m7 homo sapien
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Q55t78 homo sapien
Q55t78 homo sapien
Q53t78 homo sapien
Q55t78 mus musculu
Q55b14 mus musculu
Q4vxc6 homo sapien
Q595h4 mus musculu
Q4vxc6 homo sapien
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Result No.

Score

2814.5 2814.5 2773 2761.5 2721 2721 2634 1957.5 1957.5

1895 1683.5 1680.5 1680.5 1680.5 1673.5 1673.5 1673.5 1679.5 1669.5 1669.5 1669.5 1669.5 1669.5

Database :

Minimum DB Maximum DB

Title: Perfect score:

Run on:

Scoring table: Sequence:

45	44	43	42	41	40	39	38	37	36	35	34	33	32
1590.5	1611	1617	1629	1630.5	1657.5	1659	1660.5	1663.5	1663.5	1665	1667	1667	1667.5
39.5	40.0	40.1	40.4	40.5	41.1	41.2	41.2	41.3	41.3	41.3	41.4	41.4	41.4
1584	1576	1097	1670	1671	628	1100	1816	1695	1690	1103	1120	1103	1816
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UN104_CAEEL	Q61GI3_CAEBR	KIF1C_RAT	Q8MLF6_DROME	Q9NBL1 DROME	Q3UY61_MOUSE	Q8VI89 MOUSE	KIF1B_MOUSE	KIF1A MOUSE	KIF1A_HUMAN	Q5U618_HUMAN	Q6A011 MOUSE	KIF1C HUMAN	KIF1B_RAT
P23678 caenorhabdi	Q61gi3 caenorhabdi					Q8vi89 mus musculu							O88658 rattus norv

ALIGNMENTS

유 성	B 8	B 8	3 00	10-01-00-00-00-00-00-00-00-00-00-00-00-0	1
121 YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180 	61 AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120 	1 MSGGGNIKVVVRVFFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK 60 	Query Match 98.4%; Score 3966; DB 2; Length 786; Best Local Similarity 98.9%; Pred. No. 4.6e-194; Matches 775; Conservative 2; Mismatches 7; Indels 0; Gaps 0;	OSIUUS THELA OSIUUS THELA OSIUUS THELA PRELIMINARY; PRT; 786 AA. AC Q6IUUS; OS OSIUU-2004, integrated into UniProtKB/TrEMBL. DT 05-JUL-2004, sequence version 1. DE Unc104/KIF1A-like protein (Fragment). E Unc104/KIF1A-like protein (Fragment). OS Thermomyces lanuginosus (Humicola lanuginosa). OS ENKATyota; Pung; Ascomycota; mitosporic Ascomycota; Thermomyces. RN 11	

ч. Ж.,

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Q4X048 ASPFU
Q4X048 ASPFU
Q4X048 ASPFU
ID 043048;

AC Q4X048;

D7 Q5-JUL-2005, integrated into UniProtKB/TrEMBL.
D7 O5-JUL-2005, sequence version 1.
D7 O5-JUL-2005, entry version 6.
D7 O7-MAR-2006, entry version 6.
D8 Kinesin family protein.
GN ORFNames-Afu2g14730;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fingi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CR RA RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
RX Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett C.,
RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett C.,
RA Arroyo J., Berriman M., Edorova N.D., Feldblyum T.V., Fischer R.,
RA Arroyo J., Berriman M., Fedorova N., Fedorova N., Folscher R.,
RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
RA Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen
                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RE STRAIN-A£293 / CBS 101355 / RGSC A1100;

X PubMed=16372009; DDI=10.1038/nature04332;

X Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,

Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,

A Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,

A Arroyo J., Berriman M., Collins M., Coulsen R., Davies R., Dyer P.S.,

A Arroyo J., Berriman M., Collisen M., Coulsen R., Devr P.S.,

Ra Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,

Ra Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,

Ra Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,

Ra Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

Rose Francis D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,

Ra Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,

Ra Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,

Ra Kulkarni R., Kumagai T., May G.S., Miller B.L., Mohamoud Y., Molina M.,

Ra Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
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||KGFVGLTTPKKMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFYARR
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Best Local S
Matches 636
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RGO; GO:0005875; C:microtubule associated complex; IEA
GO; GO:0005524; F:Afrb binding; IEA.
GO; GO:0003777; F:microtubule motor activity; IEA.
RGO; GO:00037018; P:microtubule-based movement; IEA.
R InterPro; IPR001752; kinesin_motor.
R InterPro; IPR001849; pH.
R InterPro; IPR001193; PH_type.
R InterPro; IPR001193; PH_type.
R Ffam; PF00225; Kinesin; 1.
R Pfam; PF00225; Kinesin; 1.
R Pfam; PF00225; Kinesin; 1.
R Pfam; PF0023; PH; 1.
R PFANT'S; RM0013; PH; 1.
R PRINT'S; RM0013; PH; 1.
R PROSITE; PS00441; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00441; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00041; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00041; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00041; KINESIN_MOTOR_DOMAIN1; 1.
R PROSITE; PS00043; PH_DOMAIN; 1.
Complete proteome.
1632 AA; 182726 MW; 1CAED6825E77444D CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U., Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Ronning C.M., Rotter S., Salzberg S.L., Sanchez M., Rodriguez S., Sanchez M., Rotter S., Salzberg S.L., Sanchez M., Squares S., Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K., Machida M., Hall N., Barrell B.G., Denning D.W., Machida M., Hall N., Barrell B.G., Denning D.W., "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus funigatus.";
Nature 438:1151-1156(2005).

-i- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKEHGVIPRICODMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY
                                                                                                             HAVVNEDPNARMIRELKEELAQLRAKL---
                                                                                                                                  HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGG-PVEESYPPDTPLEKQIV
                                                                                                                                                                                                                     KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAFDRSYWSFDKNAPNYAGQDNLFADLGVPLLDNAFQGYNNCI FAYGQTGSGKSYSMMGY
                                                                                                                                                                                                KKKNASMVPYRDSILTWLLKDSLGGNSMTAMIAAISPADINFDETLSTLRYADSAKRIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Mismatches
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; DB 2;
2.5e-155;
ches 73;
                                                                                                             -GGGSTAGAAGGMPAEEYYPPDTPLEKQMV
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A Galagan J.E., Calvo S.E., Comoo C., Ma L.-J., Wortman J.R.,
A Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
A Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,
A Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,
A Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
A Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
A Archer D. B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
A Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
A Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
A Caddick M., Hynes M., Barren B.W.;
RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
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RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
CC - CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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26-APR-2005, integrated into UniProtKB/TrEMBL.
26-APR-2005, sequence version 1.
26-APR-2006, entry version 9.
17-MAR-2006, entry version 9.
18-Pypothetical protein.
28-Pypothetical protein.
29-Pypothetical protein.
20-Pypothetical protein.
20-Pypot
                                                                                                         EMBL; AACD
GO; GO:000
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Interpro;
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                    50; GO:0005875; C:microtubule associated co

50; GO:0005524; F:ATP binding; IEA.

50; GO:0003777; F:microtubule motor activit

50; GO:0007018; P:microtubule-based movement

interpro; IPR001253; FHA.

interpro; IPR001253; FHA.

interpro; IPR001949; PH.

interpro; IPR001949; PH.

interpro; IPR011993; PH_type.
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PRINTS; PR00380; KINESINHEAVY.

SMART; SM00129; KISG; 1.

SMART; SM00123; PH; 1.

PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50003; PH_DOMAIN; 1.

Hypothetical protein.

SEQUENCE 1630 AA; 182784 MW; 85AD0AF238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAFDRSYMSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY
                                                                                                                                                                                                                                                                                                        RREAVSA - - GMDPDRLAHMPDDELDALFENVQNVRANRRGLLENEEDSDSLSSYPIRDKY
                                                                                                                                                                                                                                                                                                                                                                                                                    RVEQSILRHSVTTSQLASPAPGKAHERNVSKA-SDLDWDSSRADSPMGFQRGRESDWFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHCKFENVDNVVTILPSEGAAVMVNGVRVDKPKRLKSGYRIILGDFHIFRFNHPQEARAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKGF IGLSTPKKMPHLVNLSDDPLLAECLVYNLKPGVTHVGNMDQGNHVEIRLNGSKILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIQQPDGTIKKVSKAEIVEQLNQSEKLYKDLNQTWEEKLIKTEQIHKEREAALEELGISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAVVNEDPNARMIRELKDELAQLRAKLGGGAAGGATAGAAGGVVADEVYPPDTPMEKQMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-KKGKQVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFDETLSTLRYADSAKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFBETLSTLRYADSAKRIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSTGPYVEDLAKLAVRSFEEIENLMDEGNKARTVAATNMNETSSRSHAVFTLMLTQKRHD
                                                                                                                                                                                     MSNGTI DNFSLDTAI IMPGTPRHGDEDATLQSVRQDMQRQLERQKEQYLDKLRESEASPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKEYGVIPRICQDMFERIRKIQEDKNLTCTVEVSYLEIYNERVRDLLNPSNKGNLKVREH
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Pred. No. 7.
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184 181 124 121 64 5

483 480 423 420 363 361 304 301 244

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Q75784_NEUCR
ID Q75784;
AC Q75784;
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AC Q75784;
AC Q75784;
DT 15-DEC-2003, i
DT 15-DEC-2003, i
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DT 15-DEC-2003, i
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DC Q75784;
DC Q75784;
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OS Neurospora cre
OC SURARYOLA; FUI
OC SORDATIONS-ENCUOO
OS NEUROSPORA CRE
RN NULLEOTIDE SEC
RC STRAIN-74-OR22
RN NEDLINE-225981
RN NEDLINE-225981
RN NEDLINE-225981
RN NEDLINE-225981
RN NEDLINE-225981
RN AUGUST T., Enc
RN JGF6 D., Fitz
RN JGF6 D., Fitz
RN JGF6 D., Fitz
RN JGF6 D., Fitz
RN MARCOLTE E., B.
RN JGF6 D., Fitz
RN MARCOLTE E., B.
RN WETNER-T-N, SCH
RN MARCOLTE E., B.
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CC DEMBLYGENBARK/DDBJ whole genome shotgun (WGS) entry which is CMS/JGenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                              Query Match
Best Local S
Matches 581
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Pfam; PF00169; PH; 1.

Pfam; PF00169; PH; 1.

PRINTS; PR00380; KINESINHEAVY.

SMART; SM00240; PHA; 1.

SMART; SM00229; KISC; 1.

SMART; SM00239; PH; 1.

SMART; SM00239; PH; 1.

PROSITE; PS00041; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50003; PH_DOMAIN; 1.

Hypothetical protein.

SEQUENCE 1962 AA; 214863 MW; 180ADBB5E8
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InterPro; IPR001752; kinesin_motor.
InterPro; IPR011849; PH.
InterPro; IPR011993; PH_type.
Pfam; PF00498; FHA; 1.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AABX01000301; EAA31425.1; -; Genomic_DNA. HSSP; P33173; 115S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
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STRAIN=74-OR23-1A /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005875; C:microtubule associated complex; GO:0005824; F:ATP binding; IEA. GO:0003777; F:microtubule motor activity; IEA. GO:00007018; P:microtubule-based movement; IEA.
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                                                                                                                         \vdash
                                                                                                                                                                                                      Similarity
AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                            MGGGGNIKVVVRCRPFNAREHDRGAQCIVEMRDNQTVLTTPPDAVVKGGKD-----QGQK
                                                                                                         MSGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPK
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                                                                                                                                                                                                      70.5%;
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                                                                                                                                                                            Score 2842; DE
Pred. No. 4.1e-
71; Mismatches
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                                                                 NEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDAL-----
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                                                                                                                                                        EEARAER----QEQSLLRHSVTNSQLG------SPAPGRHDRTLSKAGSDADGDSRSD
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 KEEYKDOLKTAEAANVEVEEIKKEKARMEETLMOLK 812
                                                                                                      SPAPFSRNTKESDWSFARREAAGAILGTDQNFAKLTDEELNALFEDVQRARAERVNVREG
                                                                                                                                                                                                              SRILHEHCVFENAADGTVTVIPKEGAAVMVNGKRVTEPTRLHSGYRIILGDFHIFRFNHP
                                                                                                                                                                                                                                                                  QIVSITTPDGTVKKVSKAEIAEQLNQSEKLLQDLNQTWEQKLQKTEEIHKEREAALEELG
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                        --FFGDKKSKQDASNVDVEELRQQQAQMEEALKTAK 781
                                                   DEDIESMASYPTREKYLSTGTLDNFSLDTALTMPSTPKQAETEEKLGQIRDVMQGQLDKQ
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07-FEB-2006,
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Gibberella moniliformis (Fusarium verticillioides).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=117187;
                                                                                                                                             NUCLEOTIDE SEQUENCE.

MEDLING=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7; Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.;

"A complete inventory of fungal kinesins in representative filamentous ascomycetes.";
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Copyrighted by the UniProt Consortium,
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RHSSE; P33173; 1158.

RGO; GO:0005874; C:microtubule; IEA.

RGO; GO:0005875; C:microtubule associated complex; IEA.

RGO; GO:00055875; C:microtubule motor activity; IEA.

RGO; GO:0005524; FiATP binding; IEA.

RGO; GO:0003777; F:microtubule motor activity; IEA.

RGO; GO:00007018; F:microtubule-based movement; IEA.

RGO; GO:0007018; P:microtubule-based movement; IEA.

RGO; GO:0007018; P:microtubule-based movement; IEA.

RINTERPOO; IPR001752; kinesin_motor.

Pfam; PF00498; FHA; 1.

RPfam; PF00498; FHA; 1.

RPfam; PF00498; FHA; 1.

RPFAMT; SM0019; KINESINHEAVY.

RPROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS00411; KINESIN MOTOR DOMAIN2; 1.

RPROSITE; PS0041; KINESIN MOTOR DOMAIN2; 1.

RPROSITE; PS0041; KINESIN MOTOR DOMAIN2; 1.

RROSITE; PS0041; KINESIN MOTOR DOMAIN2; 1.

RROSITE; PS0041; KINESIN MOTOR DOMAIN2; 1.
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                      ILKEHCTFENV-DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHIFRFNHPEE
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PSIFQRSGRESDWSLARREAAGAILGSDQNLTSLTDEELNALFEDVQRARAER----
                                                                                   ILHDHCTFENAPDGTVTLTPSEGASVMINGKRITEPSQLHSGYRVILGDFHIFRFNHPMB
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Best Local Similarity
Matches 575; Conserv
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InterPro; IPR001752; kinesin_motor.

InterPro; IPR001752; kinesin_motor.

InterPro; IPR011993; PH_type.

Pfam; PF00498; PHA; 1.

Pfam; PF00225; kinesin; 1.

Pfam; PF00199; PH; 1.

PRN0180; KINESINHEAVY.

SMART; SM00129; KISC; 1.

SMART; SM00129; KISC; 1.

SMART; SM00129; KISC; 1.

SMART; SM00129; KISC; 1.

SMART; SM00139; PH; 1.

PROSITE; PS000411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PS500067; KINESIN_MOTOR_DOMAIN2; 1.

PROSITE; PS50003; PH DOMAIN; 1.

PROSITE; PS50003; PH DOMAIN; 1.

SEQUENCE 1814 AA; 201181 MW; SF989F1BF2
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GO; G
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MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7; Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.; Schock complete inventory of fungal kinesins in representative filamentous ascomycetes."; Fungal Genet. Biol. 39:1-15(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005875; C:microtubule associated complex; GO; GO:0005524; F:ATP binding; IEA. GO; GO:0003777; F:microtubule motor activity; IEA. GO; GO:0007018; P:microtubule-based movement; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                       core 2773; DB 2;
red. No. 1.2e-132;
Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5F989F1BF2622BA1 CRC64;
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STRAIN-PH-1 / NRRL 31084;

A Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

A Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

A Arachchi H.M., Barna N., Bastien V.E., Camarata J., Chang J.,

A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,

A Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,

A Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

A Diaz J.S., Paro S., Ferreira P., FitzGerald M., Gage D.,

A Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D.,

A Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,

A Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,

A Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,

A Hafez N., Hagopian D., Johnson R., Jones C., Kamat M., Kamat A.,

A Liiev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A.,

A Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,

A Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,

A Manning J., Matthews C., Maucell E., McCarthy M., Meldrim J.,

A Manning J., Mathews C., Maucell E., McCarthy M., Meldrim J.,

A Manning J., Mathews C., Maucell E., McCarthy M., Meldrim J.,

A Manning J., Mathews C., Maucell E., McCarthy M., Meldrim J.,

A Manning J., Mathews C., Maucell E., McCarthy M., Meldrim J.,

A Manning J., Mathews C., Menga V., Murphy T., Naylor J., Nguyen C.,

A Manning J., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,

A Nicol R., Nielsen C.B., Norbu C., O'Connor T., Peterre N.,

A Nicol R., Nielsen C.B., Peterson K., Phunkhang P., Pierre N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4HXW9 GIBZE
Q4HXW9;
16-AUG-2005,
16-AUG-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
ORFNames=FG10189.1;
Gibberella zeae (Fusarium graminearum).
Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAECLVYNIKPGQTRVGNV--NQDTQAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGKL--TGGGGWRRGGS--PADEIYAEGTPLEKOMVTIVSSDGAVKKVSKAEITEOLNOS
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entry version 6.
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Best Local S
Matches 564
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GO; GO:0005874; F:AIP binding; IEA.
R GO; GO:0005777; F:microtubule motor activity; IEA.
R GO; GO:0007718; P:microtubule motor activity; IEA.
R GO; GO:0007018; P:microtubule-based movement; IEA.
R InterPro; IPR001752; kinesin_motor.
R InterPro; IPR001849; PH.
R Pfam; PF00295; Kinesin; 1.
R Pfam; PF00295; Kinesin; 1.
R Pfam; PF00169; PH; 1.
R Pfam; PF00169; PH; 1.
R PRINTS; PR00130; KINESINHEAVY.
R SMART; SM00129; KISG; 1.
R R SMART; SM00129; KISG; 1.
R R ROSITE; PS00013; PH; 1.
R RROSITE; PS00013; PH; DOMAIN; 1.
R RROSITE; PS00003; PH; DOMAIN; 1.
Complete proteome; Hypothetical protein.
C SEQUENCE 1793 AA; 198597 MW; 44AF342FED904207 CRC
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lander E.S.;
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                                                                                                                           DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGKEIGIVPMICQEIFKRADBIQKDGKTKCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFAFDRSYWSFDKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGABEKARKSGKTIMD-GPK
                                                                                           QQMVSITGPDGVLKKVSKAEIAEQLSQSEKLLTDLNQTWEEKLLKTEEIHKEREAALEEL
                                                                                                                                                                                                                                        IKNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGS--GGPVEESYPPDTPLE
                                                                                                                                                                                                                                                                                                                  PGKKKKGSGQVPYRDSVLTWLLKDSLGGNSMTAMIAAVSPADINFDETLSTLRYADSAKR
                                                                                                                                                                                                                                                                                                                                                                                                                               DTDTKMALEKVAKISLVDLAGSERANSTGATGARLKEGAEINRSLSTLGRVIAALADLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFAFDRSYWSFNKDDPNYAGQSNLFDDLGQPLLDNAFEGYNNCI FAYGQTGSGKSYSMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGNIKVVVRCRPFNSREIERNAQCIVEMKGNQTVITAP-----EGKGVKDSGPK
                                                                                                                                                                                                        IKNHAVVNEDANARMIRELKEELSLLRGKL---
                                                                                                                                                                                                                                                                                                                                         -GKQKKNQ-LVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 4.7e-132;
1; Mismatches 108;
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RESULT 8

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                                                 Best Local Sir
Matches 552;
                                                                                                                                                                                                                           GO; GO:0005875; C:microtubule associated complex; IEA
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003777; F:microtubule motor activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
InterPro; IPR001253; FHA.
InterPro; IPR001752; kinesin_motor.
InterPro; IPR001752; kinesin_motor.
InterPro; IPR001849; PH.
InterPro; IPR011993; PH_type.
Pfam; PF00498; FHA; 1.
Pfam; PF00498; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
Pfam; PF00159; Kinesin; 1.
                                                                          Query Match
Best Local Similarity
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Q86ZA3;
01-JUN-2003, 1
01-JUN-2003, 6
07-FEB-2006, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY230433; AAO59295.1; -; Genomic_DNA. HSSP; P33173; 115S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7; Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.; "A complete inventory of fungal kinesins in representative filamentous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cochliobolus heterostrophus (Drechslera maydis).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ascomycetes.";
Fungal Genet. Biol. 39:1-15(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=KLP8;
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                                                                                                                                            SEQUENCE
                                                                                                                                                          PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PROSITE; PS50067; KINESIN MOTOR DOMAIN2; PROSITE; PS50003; PH_DOMAIN; 1.
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         MEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDRSYWSFDKNAPNYARQEDLFQDLGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSRILHDHCSFENAADGTVTLTPSEGASVMINGKRITEPSQLHSGYRVILGDFHIFRFNH
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                                                                                                                                            1666 AA;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/TrEMBL sequence version 1. entry version 17.
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                                                 67.5%; Score 2721; DB 2; 69.8%; Pred. No. 4.9e-130; Live 77; Mismatches 116;
                                                                                                                                         186129 MW; 9F58CCCCF80F16EA CRC64;
                                       77;
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A
                                                                                             Length 1666;
                                                   Indels
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                                                   11;
RESULT 9
Q2UE08 ASPOR
Q2UE08 ASPOR PRELIMINARY; PRT; 1519 AA.

ID Q2UE08;

DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.

DT 24-JAN-2006, sequence version 1.

DT 07-MAR-2006, entry version 3.

DE Kinesin-like protein.

GN ORFNames-A0090026000806;

OS Aspergillus oryzae.

OC Enkaryota; Fungi; Ascomycota; Pezizomycotina; Eurox NCBL_TaxID=5062;

RN NCLEOTIDE SEQUENCE.

RC STRAIN=RIB 40;

RX PubMed=16372010; DOI=10.1038/nature04300;
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                                                                                                                                            HPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKD
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                                               SDWFYARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFP
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EMBL; AACP01000237; EAK87131.1; -; Genomic_DNA.

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                                                                                                                                                                                                  "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Pfam; PP00498; FHA; 1.
Pfam; PP00169; PH; 1.
PFANTS; PR00390; KINESINHEAVY.
SMART; SM00129; KISC; 1.
SMART; SM00129; KISC; 1.
PROSITE; PS5006; FHA DOMAIN; 1.
PROSITE; PS5006; FHA DOMAIN; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
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                                                                                                                                                                                                                                                                                                      QAEIRLNGSKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWDPSIPPDKQVVRYQTKTGEIKTVTKABLQEQLEQSEKIMSSLNESWEEKLTKTQEIQK
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                                                                                                      SPLPHFRGKDSDWFYARREAASAIL-GLDQKISHLTDDELDALFDDVQKARA-----
                                                                                                                                                                                            FHIFRFNHPEEARAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGD---SRSD
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----VRRGLVEDNEDSDSQSSFPVRDKYMSNGTIDNFSLDTAITMPGTPRSDDDGDALFF
                                                   SP----ASGDVDWTYARREYTMAKLNGQNVNFDNLNEEDLEKLFEDISRARSKKSMGSVL
                                                                                                                                                            FHVFRFNHPEEVRKARDR-----VRSTLALSTGEAHNETL-----IDGDLPSTRPD
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Best Local Simi
Matches 426;
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InterPro; IPR001849; PH.

InterPro; IPR0011849; PH.

InterPro; IPR0011849; PH.

InterPro; IPR0011993; PH type.

Pfam; PF00498; FHA; 1.

Pfam; PF00169; FHA; 1.

Pfam; PF00169; H; 1.

PFAMT; PR00380; KINESINHEAVY.

SWART; SW00213; PH; 1.

REPOSITE; PS0006; FHA DOMAIN; 1.

PROSITE; PS0006; FHA DOMAIN; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS000411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
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QBTG36 USTMA
QBTG36;
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GO; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002, integrated into UniProtKB/TrEMBL 01-JUN-2002, sequence version 1. 07-FEB-2006, entry version 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005875; C:microtubule associated complex; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003777; F:microtubule motor activity; IEA.
GO; GO:0007018; P:microtubule-based movement; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                            Similarity
                                                          MADSGNIKVVVRCRPMNSRERNRGASNLIEFVDQHQLILSPPNEADTK--ENSKATKKKS
                                                                                                                                                                                                  MSGGGNIKVVVRVRPFNAREIDRGAKCIVR-MEGNQTILTPPPGAEEKARKSGKTIMDGP
                 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK
                                                                                                                      MPFSFDRAY-----DEHTEQDDLFQYIGVELLQHAFNGFNTCVFAYGQTGSGKSHSMV
REHPSLGPYVEDLSKLVVASYPDIMNLMDEGNKARTVAATNMNETSSRSHAVFTLVLTQK
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                                                                                                                                                                                                                                           48.6%; Score 1957.5; DB
51.8%; Pred. No. 4.9e-91
tive 111; Mismatches 19
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Gaps

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Q55246;
Q55246;
24-MAY-2005, integrated into
24-MAY-2005, sequence versio
07-FEB-2006, entry version 5
Hypothetical protein.
ORFNames=CNBA6420;
                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus necformans var. neoformans B-3501A.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=283643;
                                                                                                                                                                                                                                    Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans esrotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databas
    EMBL; AAEY01000004; EAL23117.1; -; Genomic_DNA. GO; GO:0005875; C:microtubule associated comple GO; GO:0005524; F:ATP binding; IEA. GO; GO:0003777; F:microtubule motor activity; I
                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                         STRAIN=B-3501A;
                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRYNE
                                                                                                                                                                                           CAUTION: The sequence shown here is derived f EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                       preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS-----GKQKK----NQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETL
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InterPro; IPR001849; PH.
InterPro; IPR001849; PH_type.
InterPro; IPR011933; PH_type.
Pfam; PP00498; FHA; 1.
Pfam; PP00125; Kinesin; 1.
Pfam; PP00125; Kinesin; 1.
PRINTS; PR00130; KINESINHEAVY.
SMART; SM00129; KISC; 1.
SMART; SM00213; PH; 1.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS0041; KINESIN MOTOR DOMAIN2; 1.
PROSITE; PS0003; PH_DOMAIN; 1.
PROSITE; PS0003; PH_DOMAIN; 1.
PROSITE; PS0003; PH_DOMAIN; 1.
SMART; SMO0233; PH_DOMAIN; 1.
PROSITE; PS0003; PH_DOMAIN; 1.
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Similarity 53.0%; Pred. No. 8.4e-90;
20; Conservative 99; Mismatches 190; Indels
                                                                                                                                                      ARREAASAILGLDQKISHLTDDELDALFDDVQKARAVRRGLVEDNEDSDSQSSFFVRDKY
                                                                                                                                                                                                                                                          RAERQEQSLLRHSVTNSQLGSPAPGRHDRTLSKAGSDADGDSRSDSPLPHFRGKDSDWFY
                                                                                                                                                                                                                                                                                                                                KEHCTFENVDNVVTIVPNEKAAVMVNGVRI--DKPTRLRSGYRIILGDFHIFRFNHPEEA
                                                                                                                                                                                                                                                                                                                                                                                                              IEKGFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRLNGSKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSIQQPDATVKKMSKAEIVEQLNQSEKLYRDLNQTWEEKLAKTEEIHKEREAALEELGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGFVEESYPPDTPLEKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTL--TLTQKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEHGVIPRICQDMFRRIN-ELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDKSYWSAGPKDDPKYASQQTLYEDLGADLLDHSFEGFNTC1FAYGQTGSGKSYSMMGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG
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        QQAQMEEALKTA
                                                  LSNPWAGPGQTATMTSNSLATPV--
                                                                                           MSN-----
                                                                                                                                                                                                                                                                                                                                                                                      IDTNMVGVHAPQNHPSLVNLNEDPLMSECLIYQIKPGTTIAGAVDED-KAHIKLSGTHIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTHAIVNEDPNAKLIRELKEELELLRSRVLMSGLSD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNKRKKEEHVPYRDSVLTWLLKESLGGNSKTAMIAAISPAD--YEETLSTLRYADAAKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEKGIIPLTTSELFRRIEARMGSDVNLSYTVEVSYIEIYNEKVRDLLNPKNKGNLRVREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGNIKVVVRCRPLNAREIARGSKELIRMEGSQTILDPP---EATGGASSKAIEKKPMIFS
                                                                                                                                                                                                                                                                                                   PEHCSFTNDEGVVTIEAMPDARTFVNGKRVPPNSPVKLLNGFRVILGDSHVFRFNDPAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTYITKEGEIRKVTKLELQDQLEASEKLMESLNLTWEEKLQKTQAIHIEREKALEELGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSLGPYVEDLSRLVVENYTQMMTLMDEGNKARTVASTNMNETSSRSHAVFTLVVSLTQKR
                                                                                                                                                                                                                   LRISSSTDENGSLTPG-
                                                                                         -GTIDNFSLDTAITMPGTPRSDDDGDALFFGDKKSKQDASNVDVEEL-RQ
                                                                                                                                  ---IEKLADQDLDKLYDDILKLRTQRRRPESRMDIADFDSHFERSANP
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Pfam; PF00225; Kinesin; 1.
Pfam; PF00169; PH; 1.
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Q5KNG1;
15-FEB-2005,
                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISc; 1.
SMART; SM00233; PH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cryptococcus neoformans."; Science 307:1321-1324(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinesin, putative.
OrderedLocusNames=CNA06610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15653466; DOI=10.1126/science.1103773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JEC2
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                                                                                                                                                                                                                                                                Local Similarity
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    123
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                                                                                                                                       GGNÍKVVVRCRPLNAREÍARGSKELIRMEGSQTÍLDPP---EATGGASSKAÍEKKPMIFS
                                                                                                                                                                                   GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
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KEHGVIPRICQDMFRRIN-ELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVREH
                                            FDKSYWSAGPKDDPRYASQQTLYEDLGADLLDHSFEGFNTCIFAYGQTGSGKSYSMMGYG
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SETSAEQALHTS
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IPR001752; kinesin_motor.
IPR0011849; PH.
IPR011993; PH_type.
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                     A,
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                                                                                                                                                                                                                                                             47.0%;
                                                                                                                                                                                                                                                                                                                                     174210 MW; D4E65A002B91115B CRC64;
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                                                                                                                                                                                                                                                                Score 1895;
Pred. No. 6.
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RESULT 14

Q4VXC3 H

ID Q4VXC3 H

AC Q4VXC3;

DT 05-UUL-2

DT 07-FEB-2

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EMBL; AL358013; CA195222.1; -; Genomic_DNA SMR; Q4VXC3; 4-347. GO; GO:0005874; C:microtubule; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2005, integrated into UniProtKB/TrEMBL 05-JUL-2005, sequence version 1. 07-FEB-2006, entry version 5. Kinesin family member 1B. Name=KIF1B; ORFNames=RP4-736L20.1-003;
                                                                                                                           Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                         Dunn M.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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                                                                                                                           sortium, see http://www.uniprot.org/terms Commons Attribution-NoDerivs License
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InterPro; IPR000253; FHA.
InterPro; IPR0001752; Kinesin_motor.
Pfam; PF00498; FHA; 1.
Pfam; PF00225; Kinesin, 1.
PFRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00129; KISC; 1.
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PROSITE; PS500411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
SEQUENCE 1153 AA; 130363 MW; 6F0D8846CD283811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005875; C:microtubule associated complex; IEA. GO:0005524; F:ATP binding; IEA. GO:0003777; F:microtubule motor activity; IEA. GO:0000166; F:nucleotide binding; IEA.
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                                                 EKEEADLLLEQQRLDADSDSGDDSDKRSCEESWKLITSLREKLPPSKLQTIVKKCGLPSS
                                                                                                                                                        SGAHIKEEHCIFRSERSNSGEVIVTLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNHV
                                                                                                                                                                                                                           LGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLVYNIKPGQTRVGNVNQDTQAEIRL
                                                                                                                                                                                                                                                                                                                                                                                                                          DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVSK
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GKKREPIKMYQIPQRRRLSKDSKWVTISDLKIQAVKEICYEVA-LNDFRHSRQEIEALAI
                                                                                                                         FRENHPEEARAER-----
                                                                                                                                                                                   NGSKILKEHCTFENV-----DNVVTIVPNEKAAVMVNGVRIDKPTRLRSGYRIILGDFHI
                                                                                                                                                                                                                                                                 LTSVTSIQ--ERIMSTPGGEEAIERLKESEKIIAELNETWEEKLRKTEAIRMEREALLAE
                                                                                                                                                                                                                                                                              CNAVINEDPNAKLVRELKEEVTRLKDLLRAQGLGDIIDTSMGSLT--SSPSSCSLSSQVG
                                                                                                                                                                                                                                                                                                                                            NHAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGGGGGGGGGGGFVEESYPPDTPLEKQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
                       -----PLPHFR--GKDSDWFYARREAASAILGLDQKISHLTD-----DELDALFD
                                                                             APGRHDRTLSKAGSDADGDSRSDS-----
                                                                                                       FRENHPEQARAEREKTPSAETPSEPVDWTFAQRELLEKQGIDMKQEMEKRLQEMEILYKK
                                                                                                                                                                                                             MĠVAÍREDGĠTLĠVFSPKKTPHĹVNĹNEĎPĹMSEČĹĹŶYĬKDĠIŤŔVĠQADAERRQDÍVĹ
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43.6%; Pred. No. 1.2e-77;
tive 137; Mismatches 235;
                                                                                                                              ------QEQSLLRHSVTNSQ------LGSP
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Best Local S
Matches 355
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Pfam; PF00225; Kinesin; 1.
Pfam; PF00165; PH; 1.
Pfam; PF00169; PH; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00240; FHA; 1.
SMART; SM00233; PH; 1.
SMART; SM00233; PH; 1.
SMART; SM00233; PH; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
PROSITE; PS50003; PH DOMAIN; 1.
SEQUENCE 1797 AA; 201951 MW; 370ACF5BBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005875; C:microtubule associated compl
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003777; F:microtubule motor activity;
GO; GO:0007018; P:microtubule-based movement;
InterPro; IPR000253; FHA.
InterPro; IPR001752; kinesin_motor.
InterPro; IPR001849; PH.
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"Identification of splicing variants of KIF1Bbeta.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005, integrated into UniProti
19-JUL-2005, sequence version 1
07-FEB-2006, entry version 6.
Kinesin family member 1Bbeta isoform
Name=KIF1Bbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB088212; BAE02545.1; -; mRNA
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Q4R9M8;
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HUMAN
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| HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                   FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ
                                                                                                                                                                                                                               FDRSYMSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG
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                                                                                         EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
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Maximum Match 100%
Listing first 60 summaries
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Perfect score:
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermomyces lanuginosus kinesin motor protein TL-gamma
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                                                                                                                                                                                                                   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inflammation; chemotinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-dependent, plus end-directed microtubule motor protein that is a member of the unc-104 family and kinesin superfamily. The invention provides TL-gamma nucleic acids (see AXX87656), proteins and antibodies, and methods of screening for TL-gamma modulators potentially useful for treating hyphal fungal infections and diseases caused by mutated TL-gamma, e.g. neurodegeneration involving anterograde axonal transport, such as Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral sclerosis. Detection of TL-gamma allows differentiation between hyphal
                                                                                          26-JUL-2001
                                                                                                                                                                    Homo
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               23-DEC-1999;
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19-OCT-2000;
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                                                                                                                                                                                                                                                             175
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Wang Z,
Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSAK 357
                                                                                                                                                                                                                                                                                  REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
                                                                                                                                                                                                                                                                                                                                    KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 174
                                                                                                                                                                                                                                                                                                                                                            YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                     FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                          DSGPNKNKKKKTDFI PYRDSVLTWLLRENLGGNSRTAMVAALSPAD!
                                                                                                                                                                                    RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM
                                                                                                                                                                                                                     WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM
                                                                                                                                                                                                                                                             REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAÅTNMNETSSRSHÅVFNIIFTQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG
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Wehrman T,
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115 120 57 63

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful cC in gene therapy. A composition containing a polypeptide or polynucleotide cC in gene therapy. A composition containing a polypeptide or polynucleotide cC in gene therapy. A composition containing a polypeptide or polynucleotide cC in gene therapy. A composition containing a polypeptide or polynucleotide cC cC in gene therapy. A composition containing a polypeptide or polynucleotide cC system, such as peripheral nervous injuries, peripheral neuropathy and cC localised neuropathies and central nervous system diseases, such as cC Alzheimer's, Parkinson's disease, Huntington's diseases, such as cC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic cc utilisation of the activity such as: Immune system suppression, cC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, caseays for receptor activity, arthritis and inflammation, leukaemias and cC c.N.S disorders. Note: The sequence data for this patent did not form compared the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, as central nervous system injuries.
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; 2000US-0052317.
; 2000US-00598042.
; 2000US-00620312.
; 2000US-00633450.
; 2000US-00632191.
; 2000US-00693036.
; 2000US-00727344.
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  58;
Score 1152; DB 4;
Pred. No. 8.8e-105;
8; Mismatches 56;
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Xu (
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                                                 Length 421;
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  Indels
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Zhang J,
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                                                                                                                                                                                                                                                                                                                         CC The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorders, gastrointestinal disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the companion, but was obtained in electronic format directly cc from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                               Query Match
Best Local S
Matches 226
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Harthsborne TA, Suchorolski MT, Altus CM, Pitte SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietz
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                          Sequence 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2002; 2002US-0410259P
12-SEP-2002; 2002US-0410260P
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DB; ACN42303.
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                                                                               4
                                                                                                                                                                             Similarity
                GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET--
                                                                         GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page; 190pp; English
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                                                                                                                                           62.8%; Score 1152; DB 8; 62.1%; Pred. No. 8.6e-104; tive 58; Mismatches 56;
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N-PSDB;
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated
                                                                                                                                                                                                                                       Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy T Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gers Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Ki Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Patury S, Shi X, Suarez CJ;
                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                          Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                  Harthshorne TA,
                                                                                                                                                                                                                                                                                                                                                     Schmidt JP,
                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2002;
12-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                        in gene mapping.
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DB; ACN42302.
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pht RJ, Bruns CM, Marjanovic MM, Shen F;

Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

Suchorolski MT, Banville SC, Reddy TP;

Panesar IS, Banville SC, Reddy TP;

Au AP, Gerstin EH;
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                 Schmidt
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12-SEP-2002;
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2002US-0410260P
              Wright RJ,
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                                          DSAK 357
                                                                                                                  SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                                                                                                                                                                                                      WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
                                                                                                                                                                                                                                                                                                                                                                                   YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLBIYNERVRDLLNPSTKGNLKV 178
                                                                                      DSGPNKNKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA
                                                                                                                                                                               RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM
                                                                                                                                                                                                                                                                       REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK
                                                                                                                                                                                                                                                                                               REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNWNETSSRSHAVFTLTLTQK 238
                                                                                                                                                                                                                                                                                                                                                           KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                               FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.8%; Score 1152; DB 8; Length 1714;
62.1%; Pred. No. 8.7e-104;
tive 58; Mismatches 56; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                               288
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RESULT 6 ABM83647 ID ABM8

ABM83647

standard; protein; 1721

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                                                                                                                                                                                                                                                          The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine CC disorder, neurological disorders, developmental disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC gene therapy. The present sequence represents a dithp protein of the cC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention.
                                                                                                                                                         Query Match
Best Local S
Matches 226
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N-PSDB;
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
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12-SEP-2002; 2002US-0410260P
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)B; ACN42299.
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Shi X,
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       52
                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping.
                                                                                                                                                                          Similarity
                             FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG
                                                                             GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET------PKSFS
                                                                                                    GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
       FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page; 190pp;
                                                                                                                                                     62.8%;
llarity 62.1%;
Conservative 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                         58;
                                                                                                                                                     Score 1152; DB 8;
Pred. No. 8.8e-104;
8; Mismatches 56;
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                                                                                                                                                                                        Length 1721;
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                                                                                                                                                         Indels
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YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178

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20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                      Tang
Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; cRS; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; drug screening; arthritis; inflammation; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide
                                                                       Novel nucleic acids and polypeptides, useful as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM40034
                                                    Example 4;
                                                                                                                                                                                                              14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                 26-JUL-2001.
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                                                                                                                                                                                                                                                                             21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                               leukaemia.
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)B; AAI59190.
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                                                                                                                                                                               HYSEQ
                                                                                                                                     Liu C,
Wang Z,
Goodrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSGPNKNKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSG-----KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM
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                                                     SEQ ID
                                                                                                                                                                                                  2000US-00488725.

2000US-00552317.

2000US-00598042.

2000US-00620312.

2000US-00620312.

2000US-006531450.

2000US-00693036.

2000US-00693036.

2000US-00693034.
                                                                                                                                                                               INC.
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                                                                                                                                              Asundi V, (
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Zhao
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RESULT 8
ABM83653
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                                                                                                                         12-SEP-2002;
12-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human diagnostic and therapeutic pprotein SEQ ID NO:3902
                    Schmidt
                                                                        (INCY-) INCYTE CORP
                                                                                                                                                                                                          12-SEP-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; human diagnostic and therapeutic polynucleotide; dithp
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              JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSAK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET------PKSFS
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2002US-0410260P
                                                                                                                                                                                                          2003WO-US028227.
              Wright
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 1696
              ŖJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.6%; Score 1149; DB 4; 61.8%; Pred. No. 6e-104; tive 59; Mismatches 56;
                 Bruns
              Š
              Marjanovic
              ₹
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PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LY;
PI Mooney EM, Delegeane AM, Pennesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gergtin EH;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI XV, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
RN PSDB; ACN42305.

XX WPI; 2004-329366/30.

DR N-PSDB; ACN42305.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful PT in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or ry in gene mapping.

XX The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human collecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, developmental disorders, endocrine considerations caused by virus, bacteria, fungi or parasite. The dithp collecules may also be used in genetic mapping, in identifying individuals consideration. Note: The sequence attained and for somatic or germline constituention. Note: The sequence data for this patent is not represented in constituent of the printed specification, but was obtained in electronic format directly form witch and similarity 61.9%; Pred. No. 8.4e-103;

Query Match

SQ Sequence 1696 AA;

PI Machana molecular weight markers, length 1696;

PI Machana molecular of the sequence specification of the constituent of the printed specification, but was obtained in electronic format directly SQ Sequence 1696 AA;

PI Machana molecular weight markers and for somatic or germline constituent of the specification, but was obtained in electronic format directly SQ Sequence 1696 AA;
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á 밁 Ś 밁 Ś 밁 Ś 밁 Ś 밁 á 밁 Ś Query Match Best Local S Matches 224 349 289 299 169 179 110 52 64 w 4 Similarity XPPQNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR ---SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADS 355 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298 YGK--EHGVIPRICQDMFRRINBLQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178 FDRSYWSFDKNAP---NYARQEDLFODLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMG 120 GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238 KQEKDQQGIIPQLCEDLFSRINDTTND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV 168 FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG 109 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK 62.3%; Score 1142; I larity 61.9%; Pred. No. 8.4e Conservative 59; Mismatches 2; DB 8; 8.4e-103; Indels 22; 51

RESULT 9 ABM83652 ID ABM8

ABM83652

standard; protein; 1697

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                                                                                                                                                                        Matches
                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harrison
Mooney EM, Derey
Stevens KA, Blanchard J
Peralta CH, Anderson SF
Peralta CH, Spiro PA,
Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
                                                                                                                                                                                                                                      Sequence 1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human diagnostic and therapeutic pprotein SEQ ID NO:3901
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12-SEP-2002; 2002US-0410260P
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 121
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                               52
                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kwong M, 1
S, Shi X,
                                                                                                                                     4
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN42304
                                                   FDRSYWSFDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSNMG
                                                                                                                     GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
YGK--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
                               FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG
                                                                                                 GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKET-----PKSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wing You, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
ng M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzes
Shi X, Suarez CJ;
                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ight RJ, Bruns CM, Marjanovic MM, Shen F;
Suchorolski MT, Altus CM, Pitts SJ, Elder LY
Panear IS, Banville SC, Reddy TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                    62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                    Score 1142;
Pred. No. 8
                                                                                                                                                                     Mismatches
                                                                                                                                                                     3.4e-103;
1es 57;
                                                                                                                                                                                                      DB
                                                                                                                                                                                                    8
                                                                                                                                                                                                   Length 1697;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy or
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                                                                                                                                                                   Gaps
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                              109
                                                               120
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RESULT 10
ABM83649
                                                      The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski T, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietz
Patury S, Shi X, Suarez CJ;
autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or
                                                                                                                                                                                                                                                                 Claim 27;
                                                                                                                                                                                                                                                                                                                        New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human diagnostic and therapeutic pprotein SEQ ID NO:3898
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)B; ACN42301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
                                                                                                                                                                                                                                                              Page; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350
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2002US-0410260P
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                                                                                                                                                                                                                                                              English.
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                                                                                         Harthshorne
                                                                                                                Schmidt JP,
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12-SEP-2002;
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               Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder L
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gersti
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL
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2002US-0410260P.
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Pred. No. 8
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sJ. Elder LV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lagace RE, Spiro PA, Stewar Xu Y, Kwong M, Policky JL, Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1722 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in gene mapping.
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                                                                                                                                                                          WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
                                                                                                                                                                                                                                                                                                        KQEKDQQGIIPQLCEDLFSRINDTIND-NMSYSVEVSYMEIYCERVRDLLNPKNKGNLRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
AK 350
                                    AK 357
                                                                          XPPQNKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADR
                                                                                                                                                        RHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM
                                                                                                                                                                                                                                  REHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQK
                                                                                                                                                                                                                                                      REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
                                                                                                                                                                                                                                                                                                                                                                                      FDYSYWS--HTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart EA, Wingrove J,
ky JL, Hurwitz BL, Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1142; DB 8;
Pred. No. 8.6e-103;
9; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vitt UA, Ki
Jackson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1722;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gietzen D;
                                                                                                                                                                                                                                    228
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Human diagnostic and therapeutic pprotein SEQ ID NO:3920

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine CC disorder, neurological disorder, developmental disorder, endocrine CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC polymorphisms, as molecular weight markers, and for somatic or germline CC polymorphisms, as molecular weight markers a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence represents a dithp protein of the CC invention.
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Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-329368/30.
N-PSDB; ACN42323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerst Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve I Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kil Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vackson JL, XY, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; Page; 190pp; English.
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12-SEP-2002; 2002US-0410260P.
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S, Shi X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping.
                                                                            KEH--GVIPRICODMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                                                                                                                         FDRSYMSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
                                                                                                                                                                                                                                                   GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
                                                                                                                                                 FDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ 111
                                                                                                                                                                                                                                                                                     GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                               EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Policky JL,
, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 1119; [
60.8%; Pred. No. 9.1e
tive 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                     ; DB 8;
9 1e-101;
hes 63;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 1199;
                                                                                                                                                                                                                                                                                                                                                          Indels
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Shen F;
Start Elder LV;
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á 밁

Conservative

5'9;

Indels

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Gaps

5

GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63

GASVKVAVRVRPFNSRETSKESKCIIOMQGNSTSIINPKNPKE---

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AAB36227
ID AAB36
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Query Match
Best Local Similarity
Matches 220; Conserv
                                                                                                                                Sequence 1816
                                                                                                                                                                              The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIF1B and KIF1B proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease diagnosis and population studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 46; Page 189-192; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; kinesin-like protein; HKLP; KIF1; cell division; cancer; intracellular transport; neurological disorder; infertility; biallelic marker; spontaneous abortion; neonatal chromosome disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kinesin-like protein HKLP SEQ
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                                61.0%;
Score 1119; DB 3;
Pred. No. 1.8e-100;
9; Mismatches 63;
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RESULT 14
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                                      The invention provides a human kinesin-associated gene encoding a protein having a motor domain and another protein encoded by the human kinesin-associated gene having no motor domain. The genes are useful for the diagnosis and treatment of human neuroblastoma, and judgement of prognosis of this disease. Also provided are probes and primers hybridising to part of the KIFIB-beta gene, useful for diagnosing neuroblastoma in which the gene sequence is detected in tissue samples. The present sequence represents a human kinesin-associated protein having
       Sequence 1823 AA
                                                                                                                                                                               Gene
                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                            (HISM )
                                                                                                                                             Claim
                                                                                                                                                                                                                                      Nakagawara
                                                                                                                                                                                                                                                                                             29-SEP-2000; 2000JP-00300247.
                                                                                                                                                                                                                                                                                                                    01-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human kinesin-associated protein having motor domain.
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                            present sequence motor domain
                                                                                                                                                                  diagnosis
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                                                                                                                                                                                                                                                          HISAMITSU PHARM CO LTD CHIBA PREFECTURE.
                                                                                                                                                                                                      ABL40908.
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Best Local Sim
Matches 220;
                                                                                                                                                                                                 WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLIMP; kinesin-like motor protein; cytostatic; anticonvulsant; human; anti-Alzheimer; anti-Parkinsonian; antidiabetic; anti-ulcerative; cancer; immunomodulatory; antiinflammatory; anti-AIDS; antirheumatic; treatment;
                                                                        Nucleic acid sequences encoding a human kinesin-like motor (KLIMP) useful for the treatment of diseases associated wit inappropriate KLIMP expression such as cancers, neurologica and disorders of vesicular transport.
                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1998;
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DB; AAZ44744.
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                                                                                                                                                                                                                                                                                                                           INCYTE PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                            98US-00162373
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Pred. No. 1.8e-100;
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Claim

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Fig

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English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This invention describes a novel human kinesin-like motor protein (KLIMP)
C(I) which has cytostatic, anti-convulsant, anti-Alzheimer's, anti-
CC Parkinsonian, antidiabetic, anti-Creative, immunomodulatory,
CC antiinflammatory, anti-AIDS, anti-theumatic and antiarthritic activity.
C(I) and the protein it encodes may be used in the prevention, treatment
CC and diagnosis of diseases associated with inappropriate KLIMP expression
CC such as cancers, neurological disorders and disorders of vesicular
CC transport. For example, (I) (and vectors containing (I) (IV)) and the
CC decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and
CC cancers of the breast lung and prostate, neurological disorders (e.g.
CC epilepsy, Alzheimer's disease and prostate, neurological disorders (e.g.
CC endepsy, Alzheimer's disease and parkinson's disease), disorders (e.g.
CC and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g.
CC acquired immune deficiency syndrome AIDS), rheumatoid arthritis and toxic
CC shock syndrome). This sequence represents the human KLIMP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                         Key
Domain
                                                                                                                                              Human; kinesin-like motor protein; KLIMP; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; neurological disorder; epilepsy; ischaemic cerebrovascular disease; stroke; Alzheimer's disease; pick's disease; Huntington's disease; dementia; Parkinson's disease; vesicular transport disorder; cystic fibrosis; diabetes mellitus; AI Acquired Immune Deficiency Syndrome; microbial infection.
Binding-site
                                                                                                               Homo
                                                                                                                                                                                                                                                                            Human kinesin-like motor protein (KLIMP)
                                                                                                                                                                                                                                                                                                                    10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                       AAE04316;
                                                                                                                                                                                                                                                                                                                                                                                          AAE04316 standard; protein; 1103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1103 AA;
                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K--EHGVIPRICODMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP-----KQSKDAPKSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                    (first
/label= Kinesin_motor_domain
/note= "This region is speci
97. .104
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.9%; Score 1117; DB 3; 61.6%; Pred. No. 1.3e-100; co. Mismatches 62;
                     specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                     referred
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                     ij
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                     claim
                                                                                                                                                                   AIDS;
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human kinesin-like motor protein (KLIMP) from Incyte clone 1281811. KLIMP and the corresponding polynucleotide are useful for diagnosis, treatment and prevention of disorders associated with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland), neurological disorders (such as epilepsy, ischaemic cerebrovascular disease, Huntington's disease, eerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, mental disorders), and disorders of vesicular transport (such as cystic fibrosis, diabetes mellitus, AIDS (Acquired Immune Deficiency Syndrome), viral, bacterial, fungal, helminthic, and protozoal infections)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid sequences encoding a human kinesin-like motor protein (KLIMP) useful for the prevention and treatment of diseases associat with inappropriate KLIMP expression such as cancers and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                            301
                                                         231
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                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCYTE GENOMICS
FDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG
                                                                                                                                                                                                                                                                                                          GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                                       DQLTGLDSEKVSKISLVDLAGSERADSSGARGMGLKEGANINKSLTTLGKVISALADMQS
                                                                                                                                 K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE
                                                                        DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
                                                                                                                HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH
                                                                                                                                                                        EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE
                                                                                                                                                                                                                               FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ
                                                                                                                                                                                                                                                                                        GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP------KQSKDAPKSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corley NC,
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00467946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "ATP-binding site"
242. .253
/note= "Kinesin motor dom
                                                                                                                                                                                                                                                                                                                                                               60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .253
== "Kinesin motor domain signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                               Score 1117; DB 4; Pred. No. 1.3e-100;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson
                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
                                                                                                                                                                                                                                                                                                                                                                           Length 1103;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                           240
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                                                         290
                                                                                                                230
                                                                                                                                                                                                                                                             122
                                                                                                                                                                         170
                                                                                                                                                                                                                                 111
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RESULT 17 ABG72054 ID ABG72

ABG72054

standard; protein; 1103

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The invention discloses an isolated human kinesin-like motor protein (KLIMP), and the polynucleotide encoding it. Kinesins are microtubule compound protein which have an activity that includes microtubule compound that activity which generates force and directional compound. The KLIMP protein is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds KLIMP or modulates its activity and for preparing a copylyclonal or monoclonal antibody by hybridoma technology. The compound for effectiveness in altering expression of a KLIMP, for screening a compound for effectiveness in altering expression of a KLIMP, for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of KLIMP, for conditions or a disease associated with the expression of KLIMP, for conditions associated with a modulated expression of functional KLIMP are conditions associated with a modulated expression of functional KLIMP are conditions associated with a modulated expression of functional KLIMP are conditions associated with a modulated expression of functional KLIMP are conditions associated with a modulated expression of functional KLIMP are conditions of the conditions associated with abnormal vesicle trafficking such as acquired compoundeficiency syndrome (AIDS), allergic reactions, multiple sclerosis, rheumatoid arthritis and viral, bacterial, fungal, helminthic and corrotoxal infections). The sequence presented is the human KLIMP protein
Best Loc
Matches
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; kinesin-like motor protein; KLIMP; kinesin; microtuble motor protein; ATPase; force; directional movement; ac antagonist; diagnostic; transgenic; gene therapy; cancer; neurological disorder; Alzheimer's disease; Parkinson's disease; dementia; epilepsy; vesicular transport; cystic fibrosis; hypercholesterolaemia; diabetes mellitus; hyperglycaemia; hypogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal disorder; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; allergy; multiple sclerosis; rheumatoid arthritis; infection; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinesin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human kinesin-like motor protein, useful in diagnosis, prevention and treatment of cancer, neurological disorders, and disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2001; 2001US-00847874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2002
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              Local
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l Similarity
220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCYTE PHARM
                                                                      1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 1; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley NC,
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00162373.
99US-00467946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        motor protein,
                60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guegler
 59;
Score 1117; D
Pred. No. 1.3e
59; Mismatches
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 L.3e-100;
1es 62;
                                   DB
                                   9
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                                 Length 1103;
 Indels
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 16;
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Gaps
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ADG63388

ADG63388

ADG65

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ADG6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1998;
21-DEC-1999;
02-MAY-2001;
occurring amino
                                                                                                                                                                                                                                                                                                                                                                                              Tang
                          The invention relates to a new isolated polypeptide comprising the hum kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-occurring amino acid sequence that is at least 90% identical to KLIMP occurring
                                                                                                                                                                                                         New human kinesin-like motor protein and polynucleotides, useful for diagnosing, preventing or treating diseases or conditions associated aberrant protein expression, e.g. cancer, neurological disorders, All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetes; Grave's disease; Addison's disease; AIDS autoimmune haemolytic anaemia; glomerulonephritis; inflammatory bowel disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; kinesin-like motor protein; KLIMP; cancer; Alzheimer's disease; Parkinson's disease; disorder of vesicular transport; cystic fibrosis;
                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinesin-like motor protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG63388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG63388
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                YT,
                                                                                                                                                                                                                                                                                                                     2003-901054/82.
)B; ADG63389.
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                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNIKVVVRVRPENAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKQKXNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lupus erythematosus; infections;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP--
                                                                                                                                                                                                                                                                                                                                                                                                Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KKRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 98US-00162373.
; 99US-00467946.
; 2001US-00847874.
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                                                                                                                                   40pp;
                                                                                                                                                                                                                                                                                                                                                                                                Guegler
                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                   Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLIMP.
                                                                                                                                                                                                                                                                                                                                                                                                   Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQSKDAPKSFT
                                                                                   human
                                                                                                                                                                                                                    DS or
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immunogenic

fragment of

KLIMP.

or

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CC an isolated polynucleotide (NA) encoding KLIMP (appearing as ADG63389, a crecombinant polynucleotide comporising a promoter sequence operably linked to the KLIMP NA, a cell transformed with the recombinant polynucleotide, and the producing or purifying KLIMP, an isolated antibody, which specifically binds to KLIMP, methods of detecting a target polynucleotide, and the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome of the polynome
                                                                                                                                                                                      Sequence 1103 AA;
             Conservative
                                                  60.9%;
    9%; Score 1117; DB 7; Length 1103;
6%; Pred. No. 1.3e-100;
59; Mismatches 62; Indels 16
    16;
Gaps
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Query Match
Best Local Similarity
Matches 220; Conserv
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                                                                                                                              K--EHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
                                                                                       HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                                                                                                                                     FDRSYMSFDKNA-PNYARQEDLFQDLGVPLLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
                                                                                                                                                                                                             GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                           HPILGPYVQDLSKLAVTSYADIADLMDCGNKARTVAATNMNETSSRSHAVFTIVFTQRCH
           GKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
                                    DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS 300
                                                                                                                  EPGQQGIVPQLCEDLFSRVSENQ-SAQLSYSVEVSYMEIYCERVRDLLNPKSRGSLRVRE
                                                                                                                                                          FDYSYWSHTSTEDPQFASQQQVYRDIGEEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGRQ 111
                                                                                                                                                                                                 GASVKVAVRVRPFNARETSQDAKCVVSMQGNTTSIINP------KQSKDAPKSFT
- KKRKSDFI PYRDSVLTWLLKENLGGNSRTAMI AALSPADINYEETLSTLRYADRTK
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DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADMSS

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Best Local Similarity
Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                              selected compound is useful for treating, alleviating, or preventing a kifBlbeta gene-associated disease, in particular Charcot-Marie-Tooth disease type 2A. Transgenic non-human vertebrate, are useful for screening for a candidate compound for treating, alleviating, or preventing a kiflBbeta gene-associated disease. KIF1Bb DNA is useful for gene therapy and for recombinant production of polypeptides. KIF1Bb antibody is useful for affinity purification of KIF1Bb and for detecting expression of kiflBbeta gene at the protein level. The present sequence is mouse KIF1Bbeta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to KIF1Bb protein which belongs to kinesin superfamily of molecular motor proteins (KIFs). KIF1Bb is useful fiscreening for a compound binding to it. Composition comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New KIF1Bb polypeptide having motor activity that transports synaptic vesicle precursor, is useful for developing therapeutic or preventive agent for kif1Bb gene-associated diseases e.g. Charcot-Marie-Tooth
                                                                                                                                                                                                                                                                                                                                  Sequence 1770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD53964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIF1Bb protein; gene therapy; molecular motor protein; kinesin; mouse; kifBlbeta gene-associated disease; Charcot-Marie-Tooth disease type 2A; muscular; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 72-78; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2001; 2001US-0293513P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002; 2002WO-JP005226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse KIF1Bbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2003
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                                  181
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                                                                                                                                 52
                                                                                                                                                                64
                                                                                  KEH--GVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKVRE 180
                                                                                                                                                  FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122
                                                                                                                                                                                                                  GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA 63
HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKQ
                    HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
                                                               EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
                                                                                                                             FDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ
                                                                                                                                                                                               GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                60.7%; Score 1114; DB 6; 61.3%; Pred. No. 5.4e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K
                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                              Length 1770;
                                                                                                                                                                                                                                                                 Indels
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230
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RESULT 20
ADJ95088
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         16-NOV-2001;
20-NOV-2001;
20-NOV-2001;
21-NOV-2001;
28-NOV-2001;
28-NOV-2001;
29-NOV-2001;
30-NOV-2001;
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01-DEC-2001;
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11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
11-DEC-2002;
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06-NOV-2001;
09-NOV-2001;
15-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; antiinflammatory; dermatological; antiasthmatica; antiinflammatory; dermatological; antiasthmatica; antiinpemic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; hypertension; atherosclerosis; neurodegenerative disorder; alzheimer's disease; parkinson's disease; epilepsy; immune disorder; alzheimer's disease; parkinson's disease; epilepsy; immune disorder; osteoarthritis; hematopoietic disorder; inflammatory skin disorder; asthma; dyslipidemia; neurogenesis; cell differentiation; eell proliferation; hematopoiesis; wound healing; angiogenesis; chromosome mapping; tissue typing; pharmacogenomic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropi neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2002; 2002WO-US035464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel NOVX protein sequence #158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
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2001US-0334027P
2001US-033432P
2001US-033452P
2001US-0336576P
2001US-0336576P
2001US-0336576P
2001US-0336314P
2001US-0338314P
2001US-0339008P
2001US-0339008P
2001US-0339008P
2001US-0353280P
2002US-0353280P
2002US-0354392P
2002US-0354392P
2002US-0354409P
2002US-0354409P
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2001US-0348283P.
2001US-0335610P.
2001US-0335643P.
2001US-0331643P.
2001US-0331643P.
2001US-0331641P.
2001US-033461P.
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64 u 4

FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGYG 122 GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS Best Local Similarity Matches 220; Conserv

Conservative

59;

60.7%; Score 1112.5; DB 7, 61.5%; Pred. No. 7.9e-100; tive 59; Mismatches 62;

7; Length 1805;

17;

5

GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA

Query Match

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The invention relates to novel isolated polypeptides, mature forms of CC these, or a sequence that is at least 95 % identical to, or having one or conservative amino acid substitutions in the polypeptides. The CC polypeptides, nucleic acid molecules and antibodies are useful in the CC manufacture of a medicament for treating a syndrome associated with a CC human disease, preferably a NOVX-associated disorder. The nucleic acid molecules polypeptides and antibodies are useful for treating, CC preventing or diagnosing diseases such metabolic disorders, diabetes, CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension, CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders, asthma, and various CC dyslipidemias. The nucleic acids and polypeptides may also be used as CC targets for the identification of small molecules that modulate or combibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in CC generation of antibodies that bind immunospecifically to NOVX substances CC for use in therapeutic or disgnostic methods. The nucleic acids are for use in therapeutic or disgnostic methods. The nucleic acids are CC corresponds to one of the NOVX polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2002;
07-AUG-2002;
07-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2002;
17-MAY-2002;
28-MAY-2002;
17-JUL-2002;
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13-MAR-2002;
13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing, diagnosing or treating NOVX-as osteoarthritis, obesity, atherosclerosis, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS Chaudhuri A, Dipipo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV; Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Spadera SK, Spytek KA, Taupier RJ; Vernet CAM, Zerhusen BD, Zhong M;
Sequence 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 316; 800pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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23-AUG-2002;
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23-AUG-2002;
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20-AUG-2002;
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DB; ADJ95087.
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2002US-0364192P
2002US-0364227P
2002US-0383672P
2002US-0383672P
2002US-0396703P
2002US-0401552P
2002US-0401552P
2002US-0401594P
2002US-0401787P
2002US-0401787P
2002US-0401787P
2002US-0403619P
2002US-0405496P
2002US-0405496P
2002US-0406631P
2002US-0406631P
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2002US-0406631P
2002US-0406631P
2002US-0406631P
2002US-0406631P
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disease,
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The invention relates to a method (M1) of screening for modulators of a target protein. The method involves contacting the target protein with candidate agent, and determining whether the candidate agent modulates activity of target protein, where the target protein comprises a sequence that has more than 80% amino acid sequence identity to a fully defined kinesin family 14 (KIF14) protein (SEQ ID No:2) or the KIF14 motor domain sequence (SEQ ID No:3) for treating a subject with a cellular hyperproliferation, a method (M3) for treating a subject with a cellular hyperproliferation disorder, a method (M4) for identifying candidate subjects for treatment with an inhibitor of the activity of a target
                                                                                                                                                                                                           Screening for modulators of target protein e.g., kinesin family 14 protein, by contacting target protein with candidate agent, and determining whether candidate agent modulates activity of target protein.
                                                                                                                                                                                                                                                                                                                                             (ROSE-)
                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2003; 2003US-0474488P
03-JUN-2003; 2003US-0475873P
17-MAR-2004; 2004US-0553838P
                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                               Mao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-2004; 2004WO-US017234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004109290-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal-gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human KIF1B motor domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATPase modulator; kinesin family 1B; KIF1B; kinesin; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADV50414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorders; cancer; breast tumor; restenosis; cardiovascular disease; autoimmune disease; immune disorder; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADV50414 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation; musculoskeletal disease; graft rejection; inflammatory bowel disease; gastrointestinal disease; cytostatiasotropic; immunosuppressive; antiarthritic; antiinflammatory;
                                                                                                                                                                                                                                                                               2005-057663/06
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                                                                                                                                                                                                                                                                                                                                             ROSETTA INPHARMATICS LLC MERCK & CO INC.
                                                                                                                                                                                                                                                                                                             Linsley PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNETNLSTEKVVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLHAFEGYNVCIFAYGQTGAGKSYTMMGKQ
                                                                                                                                                                                  SEQ
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                                                                                                                                                                               ID NO 21; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
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CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as those disclosed in SEQ ID Nos 8, 9 or 23.

CM comprises sequences such as sampled or the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the transparence of the tran
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Best Local S
Matches 218
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291
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                                                                                                                                                                                                                                                                                                  HPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQKWH
CTSKSKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYAD
                           ---SGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYAD
                                                                                                                           DNETNLSTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN
                                                                                                                                                                    DBETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM--
                                                                                                                                                                                                                                                             HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNMNETSSRSHAVFTIVFTQKKH
                                                                                                                                                                                                                                                                                                                                                                                              EESQAGIIPQLCEELFEKIND-NCNEEMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDRSYWSF-DKNAPNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKGYSMMGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GASVKVAVRVRPFNSRETSKESKCIIQMQGNSTSIINPKNPKE-----APKSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.6%; Score 1111; DB 9; ilarity 60.7%; Pred. No. 8.2e-101; Conservative 59; Mismatches 62;
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23-MAR-2000;
11-JUL-2000;
                                                                       WO200171042-A2
                                                                                      Drosophila melanogaster.
                                                                                                           Drosophila; developmental
                                                                                                                         Drosophila
                                                                                                                                                       ABB63908;
                                                                                                                                                                     ABB63908 standard; protein; 1773
                                          23-MAR-2001; 2001WO-US009231
                                                         27-SEP-2001
                                                                                                    pharmaceutical.
                                                                                                                                         26-MAR-2002
       (PEKE ) PE
       CORP
                                                                                                                         melanogaster polypeptide
                    2000US-0191637P
2000US-00614150
                                                                                                                                        (first entry)
                                                                                                           biology;
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                                                                                                           cell
                                                                                                                          SEQ
                                                                                                           signalling; insecticide;
                                                                                                                          ID NO 18516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                        HeKiflla; human; kinesin; microtubule motor protein; cytostatic; vulnerary; antirheumatic; antiarthritic; antigout; antiinflammatory; vasotropic; neuroprotective; cytoskeletal; atherosclerossis; cancer; haematopoietic tumour; tumour metastasis; benign tumour; haemangioma; acoustic neuroma; wound healing; rheumatoid arthritis; psoriasis; Behcet's disease; gout; gouty arthritis; angiogenesis; rheumatoid arthritis; diabetic retinopathy; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventueseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                Human HsKifl3a protein sequence
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                                             vesicular
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                                                                                                                                                                                                                                                                                                                                                                                                       --KKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK 357
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Pred. No. 3e-
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Homo

sapiens

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IKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAFAFDR

Query Match Best Local Matches

Similarity

58.0%;

62;

Score 1063; DB Pred. No. 4e-95; 2; Mismatches

69; 5

10;

Gaps

66

Length 1362; Indels

Sequence

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CC This invention relates to the nucleic acid and protein sequence of a CC novel microtubule motor protein HsKifija. The protein of the invention CC may have cytostatic; vulnerary; antirheumatic; antiagout; CC antiinflammatory; vasotropic; neuroprotective activities and may act as a cytoskeletal system modulator. The HsKifija nucleic acid is useful for CC creening for modulators of HsKifija, such modulators would be useful for CC modulating cytoskeletal system for treating conditions such as abnormal Stimulation of endothelial cells (e.g., atherosclerosis), solid and CC haemangiomas, acoustic neuromas, etc., abnormal wound healing, rheumatoid CC arthritis, Behcet's disease, gout or gouty arthritis, abnormal CC angiogenesis accompanying: rheumatoid arthritis, psoriasis, diabetic CC retinopathy, etc. The sequences of the invention are useful for the CC diagnosis, treatment, or prevention of cancer, neurological and vesicular CC transport disorders. Nucleic acids encoding the kinesins are useful for the SKifija, HsKifija and its homologues are also useful as diagnostic tools in vitro. The kinesins and in particular their motor domains can be used for separation of a specific ligand from a heterologous mixture in CC also be used in the field of nanotechnology. The present sequence CC represents the human HsKifija protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                              Human microtubule motor protein, HsKif13a, useful for screening modulators of HsKif13a which are used for modulating cytoskeletal system in conditions of benign tumors and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 2; 55pp; English.
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specifically claimed in claim 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic.
The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain codir protein or complementary sequences. The polynucleotides are useful for
                                                                                                                                                                                       New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or por coagulation disorders.
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                                                                                                                                        Claim 9;
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Ma Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
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R, Wang Z,
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                                                         Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 2.1e-91;
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Chang SC; SE, Dufour GE;

ns, e.g. therapeutics

in samples

(e.g.

linked immunosorbant assay

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CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and CC proteins involved in growth and development and receptors. (I) and (II) CC may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate DITHP expression. For example, (I) and (II) CC may be used to treat disorders associated with decreased polypeptide expression by rectifying mutetions or deletions in a patient's genome, CC that affect the activity of the DITHPs, by expressing inactive proteins CC or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally, CC (I) may be used to produce the DITHPs, by inserting the nucleic acids in the complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in CC assays to detect and quantitate the presence of similar nucleic acids in CC assays to detect and quantitate the presence of similar nucleic acids in CC assays to detect and substants may be in need of restorative therapy. (II) may also be used as antigens in the production of CC antibodies against DITHPs and in assays to identify modulators of DITHP C expression and activity. The anti-DITHP antibodies and antagonists may can be approached the process of antibodies may also be used as diagnostic agents for detecting the acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acceptant acc
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24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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17-MAY-2000;
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16-MAY-2000;
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HJ, Hodgson DM,
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'sa SA, Amshey S, Dahl CR, Dam TC, Dan

Fong WT, Greenawalt LB, Hilman JL, JO

AM, Rosen BH, Russo FD, Stockdreher TK,

Yap PE, Yu JY, Bradley DL, Bratcher S

Hodgson DM, Lincoln SE, Jackson S;
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2000US-0184774P.
2000US-0184777P.
2000US-0184777P.
2000US-0184813P.
2000US-0185216P.
2000US-0185216P.
2000US-0204525P.
2000US-0204525P.
2000US-0204863P.
2000US-0205286P.
2000US-0205323P.
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TK, Daffo A;
er SR, Chen W;
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Matches 212
                                                                              05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allegies multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy, antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
                              06-SEP-2000;
06-SEP-2000;
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2000US-0229747P.
2000US-0229748P.
2000US-0229749P.
2000US-0229750P.
2000US-0229751P.
2000US-0230518P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antirheumatic; antiarthritic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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AFDRSYWSFDKNA-PMYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121

GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKVF GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF

71 62

17 63

Best Loc Matches Query Match

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al Similarity 212; Conserv

Conservative

50;

Score 1027.5; DB 5 Pred. No. 5.1e-92; 0; Mismatches 84;

<u>ن</u>

Indels Length

13;

Gaps

6

56.0%;

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The invention relates to an isolated human disease detection and CC sequence selected from 254 sequences (ABP51231-ABP5184) given in the specification, a naturally occurring polypeptide comprising a sequence (CC immunogenic fragment of (I). (I) is useful for screening a sequence (CC immunogenic fragment of (I). (I) is useful for screening a compound that (CC specifically binds (I) or modulates the activity of (I), and for (CC preparing a polyclonal or monoclonal antibody by hybridoma technology. (CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I), and for (CC polymucleotide comprising. Oligonucleotides and antibodies are useful for (CC polymucleotide comprising. Oligonucleotides and antibodies are useful for (CC polymucleotide comprising. Oligonucleotides and antibodies are useful for (CC and for purifying (I) from a sample, for detecting MDDT in a sample, for detecting with the (CC and for purifying (I) from a sample, for detecting (I), an (CC and for purifying (I) from a sample. A composition comprising (I), an (CC associated with decreased or increased expression of functional MDDT. (I) are useful for diagnosing, treating or preventing discorders are selected from a cell proliferative disorder such as arteriosclerosis, extending or transgenic anthities, psoriassis, and cancer and an (CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised or transgenic animals to model human disease, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell condition or inversion among normal, carrier or affected individuals condition or inversion among normal, carrier or affected individuals condenses.
  06-SEP-2000; 2000US-0230597P.
06-SEP-2000; 2000US-0230599P.
06-SEP-2000; 2000US-0230599P.
06-SEP-2000; 2000US-0230610P.
06-SEP-2000; 2000US-0230988P.
06-SEP-2000; 2000US-0230988P.
06-SEP-2000; 2000US-0230989P.
07-SEP-2000; 2000US-0231163P.
07-SEP-2000; 2000US-0231163P.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders earteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder \varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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Hillman JL,
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DB; ABQ72512.
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JL, Jones AL, Yu
Momiyama MG, Bra
y AM, Gerstin EH,
Marwaha R, Chen
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Yu JY, Wright RJ, Gietzen D, Li
Bradley DL, Rohatgi SD, Harris E
EH, Peralta CH, David MH, Panzer
hen AJ, Chang SC, Au AP, Inman R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rohatgi SD, Harris B;
CH, David MH, Panzer S
G SC, Au AP, Inman RR;
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05-SEP-2000;
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                     Stuart
Jones 1
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05-SEP-2000;
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                     Lincoln
Yu JY,
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                  SE, Altus
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                     CM, Dufo
Gietzen
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                  Dufour GE,
zen D, Liu
                  Chalup MS
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       が PE,
                     Hillman
, Dahl C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human diagnostic and therapeutic (dithp) copynucleotides and their associated polypeptides (DITHP polypeptides). The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, corthymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal (infections, parasitic infections, developmental disorders (e.g. anaemia, cepilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), condortine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, cortebral palsy, gastrointestinal corders (e.g. ulcerative colitis, lysinuria) and transport disorders (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences (c.g. aBG59943-ABG60220 represent human DITHP polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 211
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Marwaha
                                                                                                                                                                   ADJ69671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated polynucleotide useful
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DB; ABK71715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Page 637-639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762
                                                                                                                                                                   standard; protein; 1826
                                                                                                                                                                                                                                                              SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRYADSAK
                                                                                                                                                                                                                                                                                                       GKEHGVIPRICQDMFRRINELQKDKN--LTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178
                                                                                                                                                                                                                                              SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLRYADRAK
                                                                                                                                                                                                                                                                                                                                                                                         REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238
                                                                                                                                                                                                                                                                                                                                                                                                                               ADQPGLIPRLCSGLFER---TQKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYDHCFWSMDESVKEKYAGODIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTWMGT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF
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Peralta CH, David
Chen AJ, Chang SC,
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David MH, Panzer SR, Flores V,
g SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1020.5;
Pred. No. 2.6e
50; Mismatches
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2.6e-91;
hes 85;
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mitochondrial; human; screening assay; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LH mitochondrial encephalopathy lactic aci

lactic acidosis

and

stroke; MELAS

LHON;

diabetes

mitochondrial protein as a therapeutic target

SeqID1477

06-MAY-2004 ADJ69671;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                              CC This invention relates to novel mitochondrial targets that can be used CC for therapeutic intervention in treating a disease associated with CC altered mitochondrial function. Specifically, it refers to a method for CC identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that CC can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, CC costeoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELRS), mycolonic epilepsy cragged red fibre syndrome (MERRF) or cancer. Accordingly, these CC compositions have neuroprotective, nootropic, antidiabetic, anticarthritis, osteopathic, ophthalmological and CC cytostatic accivities. This polypeptide sequence is a human heart to the invention.
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1826 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1477; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warnock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-2003; 2003WO-US010870
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(BUCK-) BUCK INST AGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-845369/78
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                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE;
LYDAKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINESLTTLGLVISALADQ
                    WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298
                                                                                                                                                    AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYSMMGY 121
                                                                                         REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATMMNETSSRSHAVFTLTLTQK 238
                                                                                                                                 ADOPGLIPRICSGLFER - - - TOKEENEEQSFKVEVSYMEIYNEKVRDLLDPKGSRQTLKV
                                                                                                                                                                                                 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTWMGT 116
                                                                                                                                                                                                                                                                   GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKCF
                                                                                                                                                                                                                                                                                       GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF
                                                                 REHSVLGPYVDGLSKLAATSYKDIESLMSEGNKSRTVAATNMNEESSRSHAVLKITLTHT
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                    58.5%;
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                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                  Score 1016.5; DB
Pred. No. 2.7e-90;
9; Mismatches 87
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                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 1826
                                                                                                                                                                                                                                                                                                                                    87;
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   173
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RESULT 30
ADL83235
ID ADL83
XX ADL83
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                                                                                                                                                                                                                                                                                                                                                              The present invention relates to PRO proteins and their coding sequences. CC The PRO proteins are useful for diagnosing and treating a B cell related cd disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide cc antigen unresponsiveness, selective IgA deficiency, selective IgM cc deficiency, selective deficiency of IgG subclasses, immunodeficiency with thyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's companient hypogammaglobulinemia of infancy, Burkitt's companient in the companient in the companient in the companient in the companient in the companient in the companient in the companient in treating a condition that is responsive to the pRO composition, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and coding sequences are useful as hybridization probes in chromosome and companient or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               문
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Best Local (
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Antiallergic; Muscul
Gene Therapy; PRO; I
immune-mediated infl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiu H,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 437; 695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-2002; 2002US-0411392P
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                                                                                                                                                                                                       Local Similarity 58.1es 210; Conservative
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                                                                                      GDSKVKVAVRIRPMNRRETDLHTKCVVDVDANKVILNPVNTNLSKGDARGQ-----PKCF
                                                                                                                      GGGNIKVVVRVRPFNAREIDRGAKCIVRMEGNQTILTPPPGAEEKARKSGKTIMDGPKAF 62
                                                                                                                                                                                                                                                                                                                    1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
PRO; B cell related disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                 58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ζ,
                                                                                                                                                                                                       49;
                                                                                                                                                                                                    Score 1016.5; DB 8
Pred. No. 2.7e-90;
9; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s,
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                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JR,
                                                                                                                                                                                                                                                         Length 1826
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                                                                                                                                                                                                    13;
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                                                                                                                                                                                                    Gaps
                                                                                         56
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Вb	57	57 AYDHCFWSMDESVKEKYAGQDIVFKCLGENILQNAFDGYNACIFAYGQTGSGKSYTMMGT 116	, O
δ	122	122 GKEHGVIPRICQDMFRRINELQKDKNLTCTVEVSYLEIYNERVRDLLNP-STKGNLKV 178	æ
дb	117	117 ADQPGLIPRLCSGLFERTQKEENEEQSFKVEVSYMEIYNEKVRDLLDFKGSRQTLKV 173	ũ
Ş	179	179 REHPSTGPYVEDLAKLVVRSFQEIENLMDEGNKARTVAATNMNETSSRSHAVFTLTLTQK 238	60
Db	174	174 REHSVLGPYVDGLSKLAATSYKDIESLMSEGNKSRTVAATNWNEESSRSHAVLKITLTHT 233	ũ
δ	239	239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIAALADM 298	8
Вb	234	234 LYDAKSGTSGEKVGKLSLVDLAGSERATKTGAAGDRLKEGSNINESLTTLGLVISALADQ 293	ŭ
ογ	299	SSGKQKKNQLVPYRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRVADSAK 357	-
Вb	294	294 SAGK-NKNKFVPYRDSVLTWLLKDSLGGNSKTAMVATVSPAADNYDETLSTLKYADRAK 351	•
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